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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:20:16 ; Search time 22 Seconds

Sequence: 1 MTHGRSVHLHVASLILHLS... ADGELESMGFSARYNFTPGK 158 (without alignments) (without alignments)

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Post-processing: Minimum Match 0%
Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB_pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB_pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB_pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB_pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB_pep:*

6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	862	100.0	158	3 US-09-374-135-2 Sequence 2, Appli
2	260	30.2	115	3 US-09-374-135-3 Sequence 3, Appli
3	238.5	27.7	1013	2 US-08-865-650-3 Sequence 3, Appli
4	238.5	27.7	1013	2 US-09-021-287-3 Sequence 3, Appli
5	238.5	27.7	1013	3 US-09-240-473-3 Sequence 3, Appli
6	233.5	27.1	1013	2 US-08-865-650-5 Sequence 5, Appli
7	233.5	27.1	1013	2 US-09-021-287-5 Sequence 5, Appli
8	233.5	27.1	1013	3 US-08-991-408-2 Sequence 2, Appli
9	233.5	27.1	1013	3 US-09-240-473-5 Sequence 5, Appli
10	233.5	27.1	1013	4 US-09-432-710C-2 Sequence 2, Appli
11	233.5	27.1	1013	4 US-09-285-385C-20 Sequence 20, Appli
12	232.5	27.0	591	3 US-08-991-408-4 Sequence 4, Appli
13	232.5	27.0	591	4 US-09-432-473-4 Sequence 4, Appli
14	228.5	26.5	1012	4 US-09-285-385C-4 Sequence 4, Appli
15	227	26.3	901	4 US-09-285-385C-2 Sequence 5, Appli
16	226	26.2	901	4 US-08-936-135-22 Sequence 2, Appli
17	226	26.2	901	4 US-09-432-710C-22 Sequence 22, Appli
18	226	26.2	906	3 US-08-936-135-24 Sequence 24, Appli
19	226	26.2	906	4 US-09-432-710C-24 Sequence 8, Appli
20	226	26.2	909	3 US-08-936-135-8 Sequence 10, Appli
21	226	26.2	909	3 US-08-936-135-10 Sequence 8, Appli
22	226	26.2	909	4 US-09-432-710C-8 Sequence 10, Appli
23	226	26.2	909	4 US-09-432-710C-10 Sequence 12, Appli
24	226	26.2	914	3 US-08-936-135-12 Sequence 12, Appli
25	226	26.2	914	4 US-09-432-710C-12 Sequence 14, Appli
26	226	26.2	926	3 US-08-936-135-14 Sequence 14, Appli
27	226	26.2	926	3 US-09-432-710C-14 Sequence 14, Appli

RESULT 1
US-09-374-135-2

; Sequence 2, Application US/09374135
; Patent No. 6277972
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel E.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahn
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Safran, Douglas C.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
; FILE REFERENCE: 1703-017.US1
; CURRENT APPLICATION NUMBER: US/09/374,135
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095,982
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-135-2

Query Match Best Local Similarity 100.0%; Score 862; DB 3; Length 158; Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY ||||||| MTHGRSVHLHVASLILHLSGATKKPEKQTSETOKSVQCGNTWKAEGGIFTSPYPS 60
1 MTHGRSVHLHVASLILHLSGATKKPEKQTSETOKSVQCGNTWKAEGGIFTSPYPS 60

Db 1 MTHGRSVHLHVASLILHLSGATKKPEKQTSETOKSVQCGNTWKAEGGIFTSPYPS 60

QY ||||||| KUPPDRECIVYIEAAPQCIEYFDKYSIERSWECKDHIEVRDGGPFGSPIRFGCGQ 120
61 KUPPDRECIVYIEAAPQCIEYFDKYSIERSWECKDHIEVRDGGPFGSPIRFGCGQ 120

Db 61 KUPPDRECIVYIEAAPQCIEYFDKYSIERSWECKDHIEVRDGGPFGSPIRFGCGQ 120

QY ||||||| QNPVPIKSSGRFLWIKFFADGELESMGFSARVNFTPGK 158
121 QNPVPIKSSGRFLWIKFFADGELESMGFSARVNFTPGK 158

Db 121 QNPVPIKSSGRFLWIKFFADGELESMGFSARVNFTPGK 158

; APPLICANT: Afar, Daniel E.
; APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Kahan
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Saffran, Douglas C.
 APPLICANT: Jakobovits, Aya
 TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND FILED BY PROSTATE AND BLADDER CANCER CELLS
 FILE REFERENCE: 1703-017.US1
 CURRENT APPLICATION NUMBER: US/09/374,135
 PRIOR APPLICATION NUMBER: 60/095,982
 PRIOR FILING DATE: 1998-08-10
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 115
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-09-74-135-3
 Query Match 30.2%; Score 260; DB 3; Length 115;
 Best Local Similarity 43.5%; Pred. No. 1..1e-24;
 Matches 50; Conservative 20; Mismatches 37; Indels 8; Gaps 2;
 QY 52 IFTSPNPKSPKYPRECIYIEAPROCYELYDEKYSIEPSW---ECKFDHFLVR 104
 Db 1 IFPSPNFPDRPPNIDCVRVIHSRPOHQDVVKFHVFHTESTYDKDAGEECPNDFEFR 60
 QY 105 DGGPGFSPIGRGGQGQPP-VIKSSGRFLWKFADGELEMSMGFSARYNFPGK 158
 Db 61 DGRGSPSPITARCGDRMKETRAVSGTWTIPRSDDMLVYQFSAYATIVSK 115
 RESULT 3
 US-08-866-650-3
 Sequence 3, Application US/08866650
 ; Patent No. 5939321
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuhiko
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 NUMBER OF INVENTIONS: 1
 NUMBER OF PATENTS: 1
 NUMBER OF PCT: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021,287
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berzon, Bennett J
 REGISTRATION NUMBER: 37194
 REFERENCE/DOCKET NUMBER: 960296.93839
 COMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-021-287-3
 Query Match 27.7%; Score 238.5; DB 2; Length 1013;
 Best Local Similarity 39.3%; Pred. No. 1..2e-20;
 Matches 42; Conservative 25; Mismatches 39; Indels 1; Gaps 1;
 QY 47 HAGGGIFFSPNPKSPKYPRECIYIEAPROCYELYDEKYSIEPSWCKFDHIEVDG 106
 Db 779 HSPLGLITSPNWPDKYPSRKECTWVISAIPGHFIRTLAENE-FEVHQBCAYDHLTEFDG 837
 QY 107 PFGSPSPITARCGDRMKETRAVSGTWTIPRSDDMLVYQFSAYATIVSK 153
 Db 838 ETEKSPILGRGCGSKIPPLMTAGNEMFIRTSASVORKGFOATHS 884
 RESULT 4
 US-09-021-287-3
 Sequence 3, Application US/09021287
 ; Patent No. 598117
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021,287
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berzon, Bennett J
 REGISTRATION NUMBER: 37194
 REFERENCE/DOCKET NUMBER: 960296.93839
 COMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-021-287-3
 Query Match 27.7%; Score 238.5; DB 2; Length 1013;
 Best Local Similarity 39.3%; Pred. No. 1..2e-20;
 Matches 42; Conservative 25; Mismatches 39; Indels 1; Gaps 1;
 QY 47 HAGGGIFFSPNPKSPKYPRECIYIEAPROCYELYDEKYSIEPSWCKFDHIEVDG 106
 Db 779 HSPLGLITSPNWPDKYPSRKECTWVISAIPGHFIRTLAENE-FEVHQBCAYDHLTEFDG 837
 QY 107 PFGSPSPITARCGDRMKETRAVSGTWTIPRSDDMLVYQFSAYATIVSK 153
 Db 838 ETEKSPILGRGCGSKIPPLMTAGNEMFIRTSASVORKGFOATHS 884
 RESULT 5
 US-09-240-473-3
 Sequence 3, Application US/09240473

Patent No. 6397011
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuhiko
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/866, 650
 FILING DATE: 08/08/2000
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37094
 REFERENCE/DOCKET NUMBER: 960296.93839
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEX/FAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 5:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37094
 REFERENCE/DOCKET NUMBER: 960296.93839
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEX/FAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-866-650-5
 Query Match 27.1%; Score 233.5; DB 2; Length 1013;
 Best Local Similarity 40.2%; Pred. No. 4.9e-20;
 Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;
 Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;
 QY 47 HAEGGFTSPWPKPSKPPDRCIVYIIRAAPRQCIEYLDEKKISSEWSWECKEDHLYVRDG 106
 Db 779 HSPSGLITSPWPKPSKRECTWISATGHRITAFNFS-PEVQHQRCAYDHLFEDG 837
 QY 107 PFGFSPITIGRFTCGQQNPVPVKSSGRFLWIKFADGELESMGFSARYN 153
 Db 838 ETEKSILGLRGKNDPLVATGNMVFVFDASVORKGQATHS 884
 RESULT 7
 US-09-021-287-5
 ; Sequence 5, Application US/09021287
 ; Patent No. 598177
 ;
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuhiko
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021, 287
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/866, 650
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37094
 REFERENCE/DOCKET NUMBER: 960296.93839
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEX/FAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

RESULT 6
 US-08-866-650-5
 ; Sequence 5, Application US/08866650
 ;
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuhiko
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021, 287
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/866, 650
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37094
 REFERENCE/DOCKET NUMBER: 960296.93839
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEX/FAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-09-021-287-5

Query Match 27.1%; Score 233.5; DB 2; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4_9e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEKGIFTSPNVPKYPPDRECVIYEAAPROCIELYDEKYSIEPSWECKFDHIEVRDG 106

Db 779 HSPGLITSPNWPDKYPSRKECTWEISATPGHRIKLAFASE-FEIEQHQECAYDHLEVFDG 837

Qy 107 PFGFSPIGRFQGQQNPVPISSGRLEWIKFADGELESMSMGFSARYN 153

Db 838 ETEKSPILGRIGCNKIPDPPLVATGNKMFVRFVSDASVQRKGFOATHS 884

RESULT 8
US-08-991-408-2

; Sequence 2, Application US/08991408

; Patent No. 67008017

; GENERAL INFORMATION:

; APPLICANT: ARLETH, ANTHONY J.

; APPLICANT: WILLETT, ROBERT N.

; APPLICANT: ELSOURBAGY, NABIL A.

; APPLICANT: LI, XIAOTONG

; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/991,408

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/034,471

; FILING DATE: 02-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: ATG-50038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1013 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; STRANDBEDNESS: single

; MOLECULE TYPE: protein

; US-08-991-408-2

; MOLECULE TYPE: protein
; US-09-240-473-2

Query Match 27.1%; Score 233.5; DB 3; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4_9e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEKGIFTSPNVPKYPPDRECVIYEAAPROCIELYDEKYSIEPSWECKFDHIEVRDG 106

Db 779 HSPGLITSPNWPDKYPSRKECTWEISATPGHRIKLAFASE-FEIEQHQECAYDHLEVFDG 837

Qy 107 PFGFSPIGRFQGQQNPVPISSGRLEWIKFADGELESMSMGFSARYN 153

Db 838 ETEKSPILGRIGCNKIPDPPLVATGNKMFVRFVSDASVQRKGFOATHS 884

RESULT 10
US-09-132-473-2

; Sequence 2, Application US/09432473

; Patent No. 6365715

; GENERAL INFORMATION:

; APPLICANT: ARLETH, ANTHONY J.

; APPLICANT: WILLETT, ROBERT N.

; APPLICANT: ELSOURBAGY, NABIL A.

; APPLICANT: LI, XIAOTONG

; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN

; FILE REFERENCE: ATG-50038-D1

; CURRENT APPLICATION NUMBER: US/09/432,473

; CURRENT FILING DATE: 1999-11-01

; EARLIER APPLICATION NUMBER: 08/991,408

; EARLIER FILING DATE: 1997-12-16

; EARLIER APPLICATION NUMBER: 60/034,471
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-432-473-2.

Query Match Similarity 27.1%; Score 233.5; DB 4; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4.9e-20; Indels 1; Gaps 1;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEGGIFTSPNYPKYPDIRECTYIEAAPROCTIELYDFEKSISIPSWCKFDHIEVRDG 106
Db 779 HSPSGLITSPNPDKPSRKECTWEISATPGRHKLAFSE-FETEQHQEAYDHLFEDG 837

Qy 107 PFGESPILIGRCQQNPVVKSSGRFLWIKFFADGELESMGFSARYN 153
Db 838 ETEKSPBILGRLCGNKGIPDPDVATGNMKMFVRFVSDASVORKGFQATHS 884

RESULT 11
US-09-285-385C-20
; Sequence 20, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960226.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-285-385C-20

Query Match Similarity 27.1%; Score 233.5; DB 4; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4.9e-20; Indels 1; Gaps 1;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEGGIFTSPNYPKYPDIRECTYIEAAPROCTIELYDFEKSISIPSWCKFDHIEVRDG 106
Db 779 HSPSGLITSPNPDKPSRKECTWEISATPGRHKLAFSE-FETEQHQEAYDHLFEDG 837

Qy 107 PFGESPILIGRCQQNPVVKSSGRFLWIKFFADGELESMGFSARYN 153
Db 838 ETEKSPBILGRLCGNKGIPDPDVATGNMKMFVRFVSDASVORKGFQATHS 884

RESULT 12
US-09-991-408-4
; Sequence 4, Application US/08991408
; Patent No. 6008017
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: WILLETT, ROBERT N.
; APPLICANT: LI, XIAOTONG
; APPLICANT: ELSOURBAGY, NABIL A.
; APPLICANT: ELSHOURBAGY, NABIL A.
; APPLICANT: LI, XIAOTONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

RESULT 13
US-09-432-473-4
; Sequence 4, Application US/09432473
; Patent No. 6365715
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: WILLETT, ROBERT N.
; APPLICANT: LI, XIAOTONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
; CURRENT APPLICATION NUMBER: US/09/432,473
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 08/991,408
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: 60/034,471
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-432-473-4

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Query Match 27.0%; Score 232.5; DB 4; Length 591;
Best Local Similarity 40.2%; Pred. No. 3.1e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;
Match No. 43;保守性 23; 错配 40; 插入 1; 缺失 1;

QY 47 HAEGLIFTSNPYSPKYPDRECIVTEAARQCIELFYDEKYSEPSWCKFDHIEVGR 106
Db 357 HSPSGLITSPNWPDKYSPRSKRECETWEISATPGRHIKLFSE-FEIQHRECAVDHLEVFQ 415
QY 107 PFGFSPILIGRFGQQNPPVVKSGRELWIKFFADGELESMGFSARYN 153
Db 416 ETEKSPILIGRLLGNGKIPDPFLVATGMKMFVRFVSDASVORKGFQATHS 462

RESULT 14
US-09-285-385C-4
; Sequence 4, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296_96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: PRT
; ORGANISM: mouse
; US-09-285-385C-4

Query Match 26.3%; Score 227; DB 4; Length 1015;
Best Local Similarity 37.7%; Pred. No. 3.2e-19;
Matches 43; Conservative 23; Mismatches 46; Indels 2; Gaps 2;
Match No. 43;保守性 23; 错配 46; 插入 2; 缺失 2;

QY 37 KSVQCGTWTMKAEGCGTSPNYSPKYPDRECIVTEAARQCIELFYDEKYSEPSWEC 96
Db 772 KEAGCAHKLSSVEGL-ASPNWPDKYSRRECTWNISSTAGHRVLTEN-FEIQHQBC 829
QY 97 KFDHIEVGRDPFGFSPILIGRFGQQNPPVVKSGRELWIKFFADGELESMGFSAY 150
Db 830 AYDHLEMVCGPDSIAPILSRFCGSKRPDPVAVASGSSMFERFVSDASVORKGFQA 883


```

Search completed: May 18, 2004, 18:24:18
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:15:56 ; Search time 57 Seconds
(without alignments)
783.202 Million cell updates/sec

Title: US-09-887-593A-2

Perfect score: 862

Sequence: I MIFGRSVLHVASLILHLS A D G E L E S M G F S A R Y N F T P G K 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	862	100.0	158	3 AAY8294
2	851	98.7	526	6 ABB69344
3	851	98.7	523	5 ABB75587
4	802	93.0	525	7 ADC42850
5	479	55.6	130	4 ABB10345
6	479	55.6	130	5 ABB66332
7	479	55.6	141	4 AAU19919
8	470	54.5	352	4 ABB11868
9	470	54.5	487	7 ADC42852
10	470	54.5	525	4 AAM93946
11	470	54.5	525	4 AAU12228
12	470	54.5	525	4 AAB47296
13	470	54.5	525	6 ABO17672
14	470	54.5	525	6 ABBU8026
15	470	54.5	525	6 ABU66626
16	470	54.5	525	6 ABU5707
17	470	54.5	525	6 ABO2897
18	470	54.5	525	6 ABB69302
19	470	54.5	525	6 ADA45633
20	470	54.5	525	6 ADA26938
21	470	54.5	525	6 ADA66626
22	470	54.5	525	6 ADA8714
23	470	54.5	525	6 ADA61337
24	470	54.5	525	6 ADB49122
25	470	54.5	525	6 ADB27663

ALIGNMENTS

RESULT 1

ID	Description
XX	AAY82894 standard; protein; 158 AA.
AC	AAV82894;
XX	DT 25-JUL-2000 (first entry)
XX	Human brain specific protein BPC-1.
DE	
XX	KW BPC-1; oncogene; oncogenic; cancer; prostate; bladder; antibody; antisense; vaccine; detection; prognosis; drug screening; human.
KW	
XX	OS Homo sapiens.
OS	
XX	PN WO200009891-A2.
XX	PD 24-FEB-2000.
XX	PR 10-AUG-1999; 99WQ-US018250.
XX	PR 10-AUG-1998; 98US-0005982P.
XX	(URGOG-) UROGENEWS INC.
PA	(AFAR-) AFAR D E.
PA	(HUBER-) HUBERT R S.
PA	(LEONG-) LEONG K.
PA	(RAIT-) RAITANO A B.
PA	(SAFF-) SAFFRAN D C.
PA	(JAKO-) JAKOBOWITS A.
XX	PI Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC;
PI	Jakobowits A;
XX	DR WPI; 2000-20005/18.
DR	N-PADB; AAZ93040.
XX	PT New isolated BPC-1 polypeptides, useful for developing products for the diagnosis, staging, prognosis and treatment of cancers, particularly prostate or bladder cancer.
XX	PS Claim 1; Fig 1; 7pp; English.
XX	PT BPC-1 polypeptides and polynucleotides can be used for the detection of particularly useful for detecting cancers expressing BPC-1, e.g. prostate cancer or bladder cancer. Antibodies directed against BPC-1 or antisense polynucleotides can be used for treating such cancers. The BPC-1

CC polypeptides can also be used in vaccines for treating or inhibiting the development of a cancer expressing BPC-1. The polypeptides and poly nucleotides can also be used for detection, prognosis, drug screening and predicting susceptibility to developing cancer. The BPC-1 polypeptide comprises a CUB domain which is expressed in prostate and bladder carcinoma cells and which shows sequence similarity with CUB domains from other known proteins. In normal human tissues BPC-1 is only expressed in certain tissues of the brain, however, it is expressed at high levels in prostate cancer cells and bladder cancer cells.

XX SQ Sequence 158 AA:

Query Match 100.0%; Score 862; DB 3; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.8e-90; Mismatches 0; Indels 0; Gaps 0;
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGRSVLHLVAVASLILHLSGATKKGTRKQTSETOKSVOCGTWTKHAEKGIFTSPNVP 60
 1 MHGRSVLHLVAVASLILHLSGATKKGTRKQTSETOKSVOCGTWTKHAEKGIFTSPNVP 60

PR 61 KYPDPRECIVYLEAAPROCIYLFDKYSIESWECKDHLIEVRDGEGFSPIGRCQQ 120
 61 KYPDPRECIVYLEAAPROCIYLFDKYSIESWECKDHLIEVRDGEGFSPIGRCQQ 120

QY 121 QNPPIVKSSEGRFLWIKKFADGELESMGFSARVNFTPK 158
 121 QNPPIVKSSEGRFLWIKKFADGELESMGFSARVNFTPK 158

Db

RESULT 2

ABU69144 ABU69144 standard; protein; 526 AA.

XX AC ABU69144;

XX DT 02-JUN-2003 (first entry)

XX DE Human NOVX polypeptide #19.

XX KW Human; NOVX; metabolic disorder; diabetes; infectious disease; obesity; anorexia; cancer; cardiovascular disorder; asthma; neurodegenerative disorder; hematopoietic disorder; epilepsy; immune disorder; osteoarthritis; viral infection; fungal infection; helminth; protozoal infection; hypertension.

XX KW Human; NOVX; metabolic disorder; diabetes; infectious disease; obesity; anorexia; cancer; cardiovascular disorder; asthma; neurodegenerative disorder; hematopoietic disorder; epilepsy; immune disorder; osteoarthritis; viral infection; fungal infection; helminth; protozoal infection; hypertension.

XX OS Homo sapiens.

XX PN WO20020504-A2.

XX XX PD 14-NOV-2002.

XX PF 02-MAY-2002; 2002WO-US014342.

XX PR 03-MAY-2001; 2001US-0288395P.

PR 04-MAY-2001; 2001US-0288900P.

PR 07-MAY-2001; 2001US-0289087P.

PR 14-MAY-2001; 2001US-0290753P.

PR 15-MAY-2001; 2001US-0291189P.

PR 16-MAY-2001; 2001US-0291243P.

PR 18-MAY-2001; 2001US-0292001P.

PR 21-MAY-2001; 2001US-0292374P.

PR 22-MAY-2001; 2001US-0292587P.

PR 23-MAY-2001; 2001US-0293107P.

PR 29-MAY-2001; 2001US-0294110P.

PR 30-MAY-2001; 2001US-0294434P.

PR 31-JUN-2001; 2001US-0294827P.

PR 31-JUL-2001; 2001US-0308901P.

PR 17-AUG-2001; 2001US-0313388P.

PR 21-AUG-2001; 2001US-0313851P.

PR 21-AUG-2001; 2001US-0313937P.

PR 17-SEP-2001; 2001US-0322701P.

PR 17-SEP-2001; 2001US-0322802P.

PR 25-SEP-2001; 2001US-0324757P.

PR 27-SEP-2001; 2001US-0325314P.

PR 21-NOV-2001; 2001US-0325682P.

PR 03-DEC-2001; 2001US-0332129P.

PR 14-DEC-2001; 2001US-0340305P.

PR 01-MAY-2002; 2002US-00138588.

XX PA (CURA-) CURAGEN CORP.

XX PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ, Chapoval A, Edinger S, Gerlach V, Gorman L, Gunther E, Guo X, Kekuda R, Lepley DM, Li L, Liu X, Malyanik UM, Miller CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Rieper DK, Shenoy SG, Shimkets RA, Spytek KA, Taupier RJ, Vernet CAM, Voss EZ, Zerhusen BD;

XX DR WPI; 2003-103512/09.

XX N-PSDB; ACR10129.

XX PT New isolated NOVX polypeptides and Polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorder, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

XX PT Claim 2; Page 123; 340pp; English.

XX CC The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The sequences are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular disorders (e.g. Alzheimer's disease, Parkinson's disease), epilepsy, immune disorders, osteoarthritis, haematopoietic disorders, inflammatory skin disorders, asthma and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, and in the generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, and in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. Sequences ABU69126-ABU69171 represent human NOVX polypeptides of the invention.

XX SQ Sequence 526 AA;

Query Match 98.7%; Score 851; DB 6; Length 526;

Best Local Similarity 100.0%; Pred. No. 1.7e-88; Mismatches 0; Indels 0; Gaps 0;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGRSVLHLVAVASLILHLSGATKKGTRKQTSETOKSVOCGTWTKHAEKGIFTSPNVP 60
 1 MHGRSVLHLVAVASLILHLSGATKKGTRKQTSETOKSVOCGTWTKHAEKGIFTSPNVP 60

PR 61 KYPDPRECIVYLEAAPROCIYLFDKYSIESWECKDHLIEVRDGEGFSPIGRCQQ 120
 61 KYPDPRECIVYLEAAPROCIYLFDKYSIESWECKDHLIEVRDGEGFSPIGRCQQ 120

QY 121 QNPPIVKSSEGRFLWIKKFADGELESMGFSARVNFTPK 156
 121 QNPPIVKSSEGRFLWIKKFADGELESMGFSARVNFTPK 156

Do

AC ABB79587;

XX

DT 21-OCT-2002 (first entry)

XX Human CUB domain-containing protein 39362.

XX CUB domain protein; 39362; human; antiarteriosclerotic; carcipliant; cerebroprotective; hypotensive; antiarthematic; antiarthritic; antiasthmatic; neuroprotective; cytostatic; antithyroid; vasotropic; antiinflammatory; gene therapy.

XX Homo sapiens.

OS

PH

FT Key

FT Domain

FT /note= "predicted N-terminal extracellular domain"

FT 1-.23 /label= "Signal_peptide"

FT 1-.25 /note= "predicted protein kinase C phosphorylation site"

FT 23-.25 /note= "predicted protein kinase C phosphorylation site"

FT 24-.533 /label= "Mature_protein"

FT 24-.27 /note= "predicted cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT 27-.29 /note= "predicted protein kinase C phosphorylation site"

FT 31-.34 /note= "predicted casein kinase II phosphorylation site"

FT 35-.37 /note= "predicted protein kinase C phosphorylation site"

FT 41-.152 /note= "predicted CUB domain"

FT 50-.55 /note= "predicted protein kinase C phosphorylation site"

FT 129-.131 /note= "predicted protein kinase C phosphorylation site"

FT 149-.151 /note= "predicted protein kinase C phosphorylation site"

FT 172-.284 /note= "predicted N-myristoylation site"

FT 177-.182 /note= "predicted CUB domain"

FT 195-.198 /note= "predicted N-myristoylation site"

FT 241-.244 /note= "predicted casein kinase II phosphorylation site"

FT 274-.279 /note= "predicted casein kinase II phosphorylation site"

FT 285-.289 /note= "predicted N-myristoylation site"

FT 290-.328 /note= "predicted casein kinase II phosphorylation site"

FT Domain

FT Modified-site

FT /note= "predicted low density lipoprotein receptor class A domain"

FT 306-.309 /note= "predicted N-glycosylation site"

FT 313-.318 /note= "predicted N-myristoylation site"

FT 329-.332 /note= "predicted N-myristoylation site"

FT Modified-site

FT /note= "predicted casein kinase II phosphorylation site"

FT Modified-site

FT /note= "predicted N-glycosylation site"

FT Modified-site

FT /note= "predicted prokaryotic membrane lipoprotein lipid attachment site"

FT Modified-site

FT /note= "predicted N-myristoylation site"

FT Domain

FT /note= "predicted transmembrane domain"

PT Domain

FT Modified-site

FT /note= "predicted C-terminal cytoplasmic domain"

FT Modified-site

FT /note= "predicted casein kinase II phosphorylation site"

FT Modified-site

FT /note= "predicted protein kinase C phosphorylation site"

FT Modified-site

FT /note= "predicted protein kinase C phosphorylation site"

FT Modified-site

FT /note= "predicted protein kinase C phosphorylation site"

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FT /note= "predicted protein kinase C phosphorylation site"

FT Modified-site

FT /note= "predicted protein kinase C phosphorylation site"

FT Region

XX WO200259275-A2.

XX PD 01-AUG-2002.

XX PP 08-JAN-2002; 2002WO-US000275.

XX PR 08-JAN-2001; 2001US-0260286P.

XX PA (MTI-) MILLENNIUM PHARM INC.

XX PI Bandaru R;

XX DR WPI; 2002-590825/63.

XX N-PDB; ABN84415.

PS Claim 5; Page 119; 131pp; English.

CC The present sequence is the protein sequence of 39362, a novel human CUB domain-containing protein family member. The invention provides isolated CC 39362 proteins, fusion proteins, antigenic peptides and anti-39362 antibodies. It also provides isolated 39362 nucleic acid molecules, antisense nucleic acid molecules, recombinant expression vectors, host CC cells, and non-human transgenic animals, a method for identifying a compound that binds 39362, a method for modulating 39362 polypeptide activity, a method of inhibiting aberrant activity of a 39362-expressing cell using a peptide, phosphopeptide, small organic molecule or molecule, and a method of treating or preventing a disorder characterised by aberrant activity or a 39362-expressing cell, especially a cardiovascular

cell, by administering a compound that modulates the activity or expression of 39362 nucleic acid. 39362 proteins are useful in treating 39362-mediated 1 -related diseases, such as conditions involving cardiovascular disorders (e.g. atherosclerosis, myocardial infarction, aneurysm, stroke, hypertension), inflammatory disorders (e.g. rheumatoid arthritis, allergy, multiple sclerosis), and cellular proliferation or differentiation (e.g. cancer, Grave's disease, ischaemic disease). They may also be used in diagnosing, preventing or treating asthma, emphysema, chronic pulmonary disease, nephropathy, diabetes, hyperlipidaemia, infections (e.g. bacterial, viral, parasitic), hepatic injury, Parkinson's disease, or Alzheimer's disease, anxiety or cardiovascular conditions associated with interventional procedures, such as restenosis following angioplasty. 39362 proteins, protein homologues, antibodies and nucleic acids are also useful as screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays, forensic biology, monitoring clinical trials, and pharmacogenetics), and methods of treatment (e.g. therapeutic and prophylactic)

XX SQ Sequence 533 AA:

Query Match 98.7%; Score 851; DB 5; Length 533;

Best Local Similarity 100.0%; Pred. No. 1.7e-88; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGRSVLHTVASSLILHLSGATKKGTEKQTSETOKSVQCGTWIKHAEKGIFTSPNYP 60

Db 1 MIGRSVLHTVASSLILHLSGATKKGTEKQTSETOKSVQCGTWIKHAEKGIFTSPNYP 60

QY 61 KYPDPDRBCIYIEAAPROCTIELYDEKYSIERSWECKFDHIEVRDQPGFGSPICRFGCQ 120

Db 61 KYPDPDRBCIYIEAAPROCTIELYDEKYSIERSWECKFDHIEVRDQPGFGSPICRFGCQ 120

QY 121 QNPVVKSSGPIFLWIKFADGELESMGFSARVNFTP 156

Db 121 QNPVVKSSGPIFLWIKFADGELESMGFSARVNFTP 156

RESULT 4

ADC48850 ID ADC48850 standard; protein; 525 AA.

AC ADC48850; AC AC

XX DT 18-DEC-2003 (first entry)

XX DE REMAP protein #10.

XX KW Cytosstatic; Antiarteriosclerotic; Anti-HIV; Antinflammatory; Antiallergic; Antidiabetic; REMAP; Pathogenesis.

OS Homo sapiens.

XX PN WO2003027228-A2.

XX PD 03-APR-2003.

XX PP 16-JUL-2002; 2002WO-UTS022833.

XX PR 17-JUL-2001; 2001US-0306020P.

XX PR 27-JUL-2001; 2001US-0308179P.

PR 02-AUG-2001; 2001US-0309702P.

PR 10-AUG-2001; 2001US-0311476P.

PR 10-AUG-2001; 2001US-0311778P.

PR 24-AUG-2001; 2001US-0314798P.

PR 31-AUG-2001; 2001US-0316639P.

PR 07-SEP-2001; 2001US-0317996P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Lal PG, Honchell CD, Forsethe IJ, Walia NK, Tang TY, Borowsky ML;

PI Barroso I, Yue H, Warren BA, Duggan BM, Tran B, Li JX;

PI Lee EA, Baughn MR, Gorvad AE;

PI DR 2003-421156/39.

PI Richardson TW, Elliott VS, Zebardadian Y, Tran UK, Yao MG; PI Peterson DP, Luo W, Lehr-Mason PM; XX WPI: 2003-421156/39.

PT New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating or preventing disorders associated with aberrant REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or stroke.

PS Claim 1; SEQ ID NO 10; 115P; English.

CC XX The present invention relates to an isolated polypeptide. The polypeptides and polynucleotides are useful in diagnosis, treating and preventing disorders associated with aberrant expression of REMAP, such as cell proliferative, autoimmune/inflammatory, renal, neurological, cardiovascular, metabolic, developmental, endocrine, muscle, gastrointestinal, lipid metabolism or transport disorders, and viral infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acids and amino acid sequences of REMAP, in facilitating drug discovery process, and in investigating the pathogenesis of diseases or medical conditions. Expression and purification were achieved using bacterial or virus-based expression systems. The present sequence represents an REMAP protein of the invention.

CC XX SQ Sequence 525 AA:

Query Match 93.0%; Score 802; DB 7; Length 525;

Best Local Similarity 99.3%; Pred. No. 7e-83; Matches 146; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVASLILHLSGATKKGTEKQTSETOKSVQCGTWIKHAEKGIFTSPNYPKPPREC 69

Db 2 WASLILHLSGATKKGTEKQTSETOKSVQCGTWIKHAEKGIFTSPNYPKPPREC 61

QY 70 YTEAAPRQCILEYDEKYSIERSWECKFDHIEVRDQPGFGSPICRFGCQONPVIKS 129

Db 62 YTEAAPRQCILEYDEKYSIERSWECKFDHIEVRDQPGFGSPICRFGCQONPVIKS 121

QY 130 GRFLWIKFFADGELESMGFSARYNFTP 156

Db 122 GRFLWIKFFADGELESMGFSARYNFTP 148

RESULT 5

ABB10345 ABB10345 standard; protein; 130 AA.

AC ABB10345; AC AC

XX DT 10-JAN-2002 (first entry)

XX DE Human cDNA SEQ ID NO: 653.

XX KW Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.

XX OS Homo sapiens.

XX FN WO200154474-A2.

XX PD 02-AUG-2001.

XX PR 17-JAN-2001; 2001WO-US001349.

XX PR 31-JAN-2000; 2000US-017905P.

PR 04-FEB-2000; 2000US-018062P.

PR 24-FEB-2000; 2000US-018466P.

PR 02-MAR-2000; 2000US-018635P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 3-0-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-021680P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218390P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0225159P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225366P.
 PR 14-AUG-2000; 2000US-0225367P.
 PR 14-AUG-2000; 2000US-0225368P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225575P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 14-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-022688P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228024P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 05-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 14-SEP-2000; 2000US-0232080P.
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 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233397P.
 PR 14-SEP-2000; 2000US-0233398P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 26-SEP-2000; 2000US-0234998P.
 PR 27-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 02-OCT-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239337P.
 PR 20-OCT-2000; 2000US-024060P.
 PR 20-OCT-2000; 2000US-024121P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0241787P.
 PR 08-NOV-2000; 2000US-0246174P.
 PR 08-NOV-2000; 2000US-0246175P.
 PR 08-NOV-2000; 2000US-0246176P.
 PR 08-NOV-2000; 2000US-0246177P.
 PR 08-NOV-2000; 2000US-0246178P.
 PR 08-NOV-2000; 2000US-0246323P.
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 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
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 PR 08-NOV-2000; 2000US-0246534P.
 PR 08-NOV-2000; 2000US-0246535P.
 PR 08-NOV-2000; 2000US-0246536P.
 PR 08-NOV-2000; 2000US-0246537P.
 PR 08-NOV-2000; 2000US-0246538P.
 PR 08-NOV-2000; 2000US-0246539P.
 PR 08-NOV-2000; 2000US-0246540P.
 PR 08-NOV-2000; 2000US-0246541P.
 PR 08-NOV-2000; 2000US-0246542P.
 PR 17-NOV-2000; 2000US-024907P.
 PR 17-NOV-2000; 2000US-024907P.
 PR 17-NOV-2000; 2000US-024908P.
 PR 17-NOV-2000; 2000US-02492209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-02492245P.
 PR 17-NOV-2000; 2000US-0249225P.
 PR 17-NOV-2000; 2000US-02492264P.
 PR 17-NOV-2000; 2000US-02492265P.
 PR 17-NOV-2000; 2000US-0249227P.
 PR 17-NOV-2000; 2000US-0249229P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0250303P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 05-DEC-2000; 2000US-0249297P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-025097P.
 PR 05-JAN-2001; 2001US-0259678P.

XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX DR WPI; 2001-476161/51.
 XX DR N-PSDB; ABA05567.

PT Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.

XX PS Claim 11; SEQ ID NO 653; 859pp + Sequence Listing; English.

XX CC The present invention provides human cDNAs, proteins and related genomic

Db	69	FDHLEVRDGPFGSPPLIDRYUGVKSPPLIRSTGFRMWWIKFSSDEELBGIGERAKYKFIPG	128
Qy	158	K 158	
Db	129	K 129	
			RESULT 7
AAU19919			
ID	AAU19919	standard; protein; 141 AA.	
AC	AAU19919;		
XX			
DT	0-4-DEC-2001	(first entry)	
XX			
DE	Novel human calcium-binding protein #28.		
XX			
KW	Human; calcium-binding protein; calcium flux; neurological disease; immune dysfunction; digestive disorder; neoplastic disease; blood disorder; infectious disease; gene therapy; immunosuppressive; antiarthritic; cytostatic; vasotropic; antibacterial; nootropic; virucide.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200155304-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001; 20001WO-US001302.		
XX			
PR	31-JAN-2000; 20000US-0179065P.		
PR	04-FEB-2000; 20000US-0186028P.		
PR	24-FEB-2000; 20000US-0184664P.		
PR	02-MAR-2000; 20000US-0186350P.		
PR	16-MAR-2000; 20000US-0189874P.		
PR	17-MAR-2000; 20000US-0190076P.		
PR	18-APR-2000; 20000US-0198123P.		
PR	19-MAY-2000; 20000US-0205151P.		
PR	07-JUN-2000; 20000US-0209467P.		
PR	28-JUN-2000; 20000US-0214886P.		
PR	30-JUN-2000; 20000US-0215135P.		
PR	07-JUL-2000; 20000US-0216647P.		
PR	11-JUL-2000; 20000US-0217487P.		
PR	11-JUL-2000; 20000US-0217496P.		
PR	14-JUL-2000; 20000US-0218290P.		
PR	26-JUL-2000; 20000US-0220963P.		
PR	26-JUL-2000; 20000US-0220964P.		
PR	14-AUG-2000; 20000US-0224518P.		
PR	14-AUG-2000; 20000US-0224519P.		
PR	14-AUG-2000; 20000US-0225213P.		
PR	14-AUG-2000; 20000US-0225214P.		
PR	14-AUG-2000; 20000US-0225266P.		
PR	14-AUG-2000; 20000US-0225267P.		
PR	14-AUG-2000; 20000US-0225268P.		
PR	14-AUG-2000; 20000US-0225270P.		
PR	14-AUG-2000; 20000US-0225447P.		
PR	14-AUG-2000; 20000US-0225757P.		
PR	14-AUG-2000; 20000US-0225758P.		
PR	14-AUG-2000; 20000US-0225759P.		
PR	18-AUG-2000; 20000US-0226279P.		
PR	22-AUG-2000; 20000US-0226681P.		
PR	22-AUG-2000; 20000US-0226868P.		
PR	01-SEP-2000; 20000US-0229344P.		
PR	01-SEP-2000; 20000US-0229345P.		
PR	05-SEP-2000; 20000US-0229505P.		
PR	08-SEP-2000; 20000US-0231141P.		
PR	08-SEP-2000; 20000US-0232080P.		
PR	08-SEP-2000; 20000US-023401P.		
PR	12-SEP-2000; 20000US-0231968P.		
PR	08-SEP-2000; 20000US-0231243P.		
PR	08-SEP-2000; 20000US-0231244P.		
PR	08-SEP-2000; 20000US-0231413P.		
PR	08-SEP-2000; 20000US-0232399P.		
PR	08-SEP-2000; 20000US-0234274P.		
PR	14-SEP-2000; 20000US-0233063P.		
PR	14-SEP-2000; 20000US-0233978P.		
PR	14-SEP-2000; 20000US-0234413P.		
PR	14-SEP-2000; 20000US-0234414P.		
PR	14-SEP-2000; 20000US-0234415P.		
PR	14-SEP-2000; 20000US-0234416P.		
PR	21-SEP-2000; 20000US-0234422P.		
PR	21-SEP-2000; 20000US-0234423P.		
PR	25-SEP-2000; 20000US-0234998P.		
PR	26-SEP-2000; 20000US-0235484P.		
PR	27-SEP-2000; 20000US-0235834P.		
PR	27-SEP-2000; 20000US-0235835P.		
PR	29-SEP-2000; 20000US-0236367P.		
PR	29-SEP-2000; 20000US-0236368P.		
PR	29-SEP-2000; 20000US-0236369P.		
PR	29-SEP-2000; 20000US-0236370P.		
PR	29-SEP-2000; 20000US-0236371P.		
PR	02-OCT-2000; 20000US-0236327P.		
PR	02-OCT-2000; 20000US-0237037P.		
PR	02-OCT-2000; 20000US-0237039P.		
PR	02-OCT-2000; 20000US-0237704P.		
PR	13-OCT-2000; 20000US-0239935P.		
PR	13-OCT-2000; 20000US-0239937P.		
PR	20-OCT-2000; 20000US-0240960P.		
PR	20-OCT-2000; 20000US-0241221P.		
PR	20-OCT-2000; 20000US-0241785P.		
PR	20-OCT-2000; 20000US-0241786P.		
PR	20-OCT-2000; 20000US-0241787P.		
PR	20-OCT-2000; 20000US-0241808P.		
PR	20-OCT-2000; 20000US-0241809P.		
PR	20-OCT-2000; 20000US-0241826P.		
PR	01-NOV-2000; 20000US-0246117P.		
PR	08-NOV-2000; 20000US-0246474P.		
PR	08-NOV-2000; 20000US-0246475P.		
PR	08-NOV-2000; 20000US-0246476P.		
PR	08-NOV-2000; 20000US-0246477P.		
PR	08-NOV-2000; 20000US-0246478P.		
PR	08-NOV-2000; 20000US-0246523P.		
PR	08-NOV-2000; 20000US-0246524P.		
PR	08-NOV-2000; 20000US-0246525P.		
PR	08-NOV-2000; 20000US-0246526P.		
PR	08-NOV-2000; 20000US-0246527P.		
PR	08-NOV-2000; 20000US-0246528P.		
PR	08-NOV-2000; 20000US-0246529P.		
PR	08-NOV-2000; 20000US-0246609P.		
PR	08-NOV-2000; 20000US-0246610P.		
PR	08-NOV-2000; 20000US-0246611P.		
PR	08-NOV-2000; 20000US-0246613P.		
PR	17-NOV-2000; 20000US-0249021P.		
PR	17-NOV-2000; 20000US-0249123P.		
PR	17-NOV-2000; 20000US-0249214P.		
PR	17-NOV-2000; 20000US-0249215P.		
PR	17-NOV-2000; 20000US-0249216P.		

PR 17-NOV-2000; 2000US-0249317P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249397P.
 PR 17-NOV-2000; 2000US-0249399P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX DR WPI; 2001-46558/50.
 XX N-PSDB; AAS31604.
 PT Isolated nucleic acid molecule encoding a calcium-binding protein is used
 PT in preventing, treating or ameliorating a medical condition.
 XX ^PS Claim 11; SEQ ID NO 116; 542PP; English.
 XX CC The present invention relates to the isolation of novel human calcium-
 CC binding proteins, and cDNA (AAS3157-AAS31654) and genomic sequences
 CC encoding for those proteins. The sequences of the invention are useful in
 CC the diagnosis, prevention and/or prognosis of diseases associated with
 CC aberrant calcium flux. Such disorders include neurological diseases (e.g.
 CC amyotrophic lateral sclerosis (ALS), immune dysfunction (e.g. severe
 CC combined immunodeficiency (SCID)), digestive disorders (e.g. irritable
 CC bowel syndrome, IBS), neoplastic disease (e.g. acquired
 CC (e.g. haemophilia), and/or infectious disease (e.g. acquired
 CC immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are
 CC also useful as screening tools to identify antagonists and/or agonists
 CC that may enhance or inhibit activities mediated by calcium-binding
 CC proteins. The polynucleotides of the invention are also useful in gene
 CC therapy. AAS19892-AAS19969 represent the novel human calcium-binding
 CC proteins. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 141 AA;

Query Match 55.6%; Score 479; DB 4; Length 141;
 Best Local Similarity 66.1%; Pred. No. 1; 4e-46;
 Matches 80; Conservative 21; Mismatches 20; Indels 0; Gaps 0;

QY 3B SWQCGTWTKHAGGIFTSPNYSKYPDPRECIIVTEAPRQTYIYDEBKISIEPSWCK 97
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 9 ARQCGIWIWRTSNGHFPASPNYPSDYPNKECILAEAPRQTYIYDEBKISIEPSWCK 68
 QY 98 FDHIEVRUGPFPSGIKGRFCGQNPVYIKSRSERFLWIKFEDGELSMGRARYNTPG 157
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 69 FDHIEVRUGPFPSGIKSPLDYCGKSPPLRSTCRFMWIKFSSEBLLEIGFRAKYSTPG 128

QY 158 K 158
 Db 129 K 129

AB11868
 ID ABB11868 standard; peptide; 352 AA.
 XX ABB11868;
 XX DT 11-JAN-2002 (first entry)
 XX DE Human secreted protein homologue, SEQ ID NO:2238.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 XX haemopoiesis regulation; tissue growth; immunomodulator; activin;
 XX inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 XX proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 XX myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 XX chronic inflammatory condition; proliferative retinopathy;
 XX atherosclerosis; coronary heart disease; arterial ischaemia;
 XX bone disorder; osteoporosis; vascular growth disorder;
 XX tissue regeneration; wound healing; infection; immune disorder;
 XX cell culture; drug screening; gene therapy; antiinflammatory;
 XX antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 XX cytostatic; osteopathic; vasorropic; cardiant; virucide; antibacterial;
 XX antifungal; vulnerary; antiulcer.
 XX OS Homo sapiens.
 XX PN WO200157188-A2.
 XX PD 09-AUG-2001.
 XX PP 05-FEB-2001; 2001WO-US003800.
 XX PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI; 2001-457740/49.
 XX N-PSDB; ABA09112.
 XX PT Human Proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX DS Claim 20; Page 268; 1963PP; English.
 XX CC sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09514 represent nucleic acids encoding them. The
 CC invention relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 giving an insight into their probable biological activities, and hence
 potential therapeutic applications. The polypeptides of the invention may
 have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haemopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 XX polypeptide of the invention.

SQ Sequence 352 AA;

Query Match 54.5%; Score 470; DB 4; Length 352;
 Best Local Similarity 54.9%; Pred. No. 5.1e-45;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVLHT--VASYLILHISGATKKGTEKQTSTOKSVQCGTWKHAEGGITSPNPKSVP 63
 Db 28 SVLKVLILTVLWVEGIAVAKQTQDGFSPLIGRQWVWRISNGHASPNSYF 87
 QY 64 PDRECYTIEAAPROCTYLEDEKYSIESPWECKEDHIEVRDGPGFSPITGRQQNP 123
 ID 88 PNKECYIILFAAPROCTYLEDEHYYIEPSFCREDHLEVRDGPGFSPSLIDRYGVKSP 147
 Db 148 PLIRSTGFRMWIKFSSDEELEGGLGRAKYSFIP 180

RESULT 9

ADC42852

ID ADC42852 standard; protein; 487 AA.

XX

AC ADC42852;

XX

DT 18-DEC-2003 (first entry)

XX

DE REMAP protein #12.

DE

XX

KW Cytostatic; Antiarteriosclerotic; Anti-HIV; Anti-inflammatory;

XX

KW Antiallergic; Antidiabetic; REMAP; Pathogenesis.

OS Homo sapiens.

XX

WO2003027228-A2.

XX

PD 03-APR-2003.

XX

PF 16-JUL-2002; 2002W0-US022833.

XX

PR 17-JUL-2001; 2001US-03060205.

XX

PR 27-JUL-2001; 2001US-0308179P.

XX

PR 02-AUG-2001; 2001US-0309702P.

XX

PR 10-AUG-2001; 2001US-0311476P.

XX

PR 10-AUG-2001; 2001US-0311553P.

XX

PR 10-AUG-2001; 2001US-0311718P.

XX

PR 24-AUG-2001; 2001US-0314798P.

XX

PR 31-AUG-2001; 2001US-0316639P.

XX

PR 07-SEP-2001; 2001US-0317996P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lal PG, Honchell CD, Forsythe IJ, Walia NK, Tang TY, Borowsky ML;

PI Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;

PI Lee EA, Baughn MR, Gorvad AE, Duggan BM, Tran B, Li JK;

PI Richardson TM, Elliott VS, ZeharJadian Y, Tran UK, Yao MG;

PI Peterson DP, Luo W, Lehr-Mason PM;

XX DR DR

WPI; 2003-421156/39.

PT New human receptors and membrane-associated proteins (REMAP), useful for

CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 XX

SQ Sequence 352 AA;

Query Match 54.5%; Score 470; DB 4; Length 352;
 Best Local Similarity 54.9%; Pred. No. 5.1e-45;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVLHT--VASYLILHISGATKKGTEKQTSTOKSVQCGTWKHAEGGITSPNPKSVP 63
 Db 28 SVLKVLILTVLWVEGIAVAKQTQDGFSPLIGRQWVWRISNGHASPNSYF 87

RESULT 10

AAM93946

ID AAM93946 standard; protein; 525 AA.

XX

AC AAM93946;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 4135.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 990P-00194486.

XX

PR 11-JAN-2000; 2000UP-00118774.

XX

PR 02-MAY-2000; 2000UP-00183765.

XX

(HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX DR WPI; 2001-54245/58.

DR N-PSDB; AAK94910.

XX PT 830 Primers useful for synthesizing full length cDNA clones and their use

PT diagnosing, treating or preventing disorders associated with aberrant
 PT expression, e.g. cancer, AIDS, atherosclerosis, hypertension or
 PT stroke.

XX Claim 1; SEQ ID NO 12; 115pp; English.

The present invention relates to an isolated polypeptide. The

polypeptides and polyribonucleotides are useful in diagnosing, treating and
 preventing disorders associated with aberrant expression of REMAP, suchas cell proliferative, autoimmune/inflammatory, renal, neurological,
 cardiovascular, metabolic, developmental, endocrine, muscle,gastrointestinal, lipid metabolism or transport disorders, and viral
 infections. These are also useful in assessing the effects of exogenous
 compounds on the expression of nucleic acids and amino acid sequences of
 REMAP, in facilitating drug discovery processes, and in investigating the
 pathogenesis of diseases or medical conditions. Expression and
 purification were achieved using bacterial or virus-based expression
 systems. The present sequence represents an REMAP protein of the
 invention.

SQ Sequence 487 AA;

Query Match 54.5%; Score 470; DB 7; Length 487;
 Best Local Similarity 54.9%; Pred. No. 8e-45; 38; Indels 2; Gaps 1;

QY 6 SVLHT--VASYLILHISGATKKGTEKQTSTOKSVQCGTWKHAEGGITSPNPKSVP 63
 Db 8 SVLKVLILTVLWVEGIAVAKQTQDGFSPLIGRQWVWRISNGHASPNSYF 67

RESULT 11

AAM93946

ID AAM93946 standard; protein; 525 AA.

XX

AC AAM93946;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 4135.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 990P-00194486.

XX

PR 11-JAN-2000; 2000UP-00118774.

XX

PR 02-MAY-2000; 2000UP-00183765.

XX

(HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX DR WPI; 2001-54245/58.

DR N-PSDB; AAK94910.

XX PT 830 Primers useful for synthesizing full length cDNA clones and their use

xx
PS Claim 8; SEQ ID NO 4135; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
CC
CC
XX
SQ Sequence 525 AA:

Query Match	54.5%	Score	470;	DB	4;	Length	525;		
Best Local Similarity	54.9%	Pred.	No.	8..8e-45;					
Matches	84;	Conservative	29;	Mismatches	38;	Indels	2;	Gaps	1;

Qy 6 SVLHI--VASLILHLISGATKKGTEKQTSETOKSVQGTWTKHARGGIFTSPNVPSPKYP 63
Db 8 SVLKVLITLVNLVEGIAVAKQKDQNGIKHIPATOCGIWRTSNGHFRASPVPDSDP 67
Db 64 PDRECIYIEAAPRCIYLFDKYSIIPSWECKFDFHIEVRDGPGFPIGRGQQNP 123
Qy 68 PRKECIVTILEAPPROTELFDEHYIPEFSFCRDFLEVRDGPGFSPSLIDRYCGVKSP 127
Qy 124 PVIKSSGRFLWIKKFADGELESSMGFSARVNITP 156
Db 128 PLIRSTGRFMWIKFSSDEELELGIFPRAKYSFP 160

RESULT 11
AAU12228
ID AAU12228 standard; protein; 525 AA.
XX
AC AAU12228;
XX DT 24-OCT-2001 (first entry)
XX DR Human PRO401 polypeptide sequence.
XX PT Human PRO401 polypeptide sequence.
XX KX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; ear-peptide; factor VIIa; gene therapy.
XX OS Homo sapiens.
PN WO200140466-A2.
XX DD 07-JUN-2001.
XX DP 01-DEC-2000; 2000WO-US032678.
XX PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028334.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030055.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0203832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Bersani M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z;
XX PI Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z;
XX DR N-PSDB; ASN21300.
XX PT Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.
XX PS Claim 12; Fig 11A; 813pp; English.
XX CC AAU12172-AAU1246 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumors by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumor necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in peritoneal cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
XX SQ Sequence 525 AA:
Query Match 54.5% Score 470; DB 4; Length 525;
Best Local Similarity 54.9%; Pred. No. 8..8e-45;
Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
Qy 6 SVLHI--VASLILHLISGATKKGTEKQTSETOKSVQGTWTKHARGGIFTSPNVPSPKYP 63
Db 8 SVLKVLITLVNLVEGIAVAKQKDQNGIKHIPATOCGIWRTSNGHFRASPVPDSDP 67
Qy 64 PDRECIYIEAAPRCIYLFDKYSIIPSWECKFDFHIEVRDGPGFPIGRGQQNP 123

Db 68 PNKECIVILEAKAPRQTCIYFDPKYSTPSWECKFDIEVRDGFSPILRGFCQNP 127
 ID AAB47296 standard; protein; 525 AA.
 XX
 AC AAB47296;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE PRO4401 polypeptide.
 XX
 KW PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte; PRO1199; PRO1556; PRO401; PRO10268; inhibition; stimulation; infiltration; mononuclear cell; eosinophil; erythema multiforme; polymorphonuclear neutrophil; PMN; antibody; immune-related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome; Skin disease; systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma; autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy; immune-mediated renal disease; demyelination; central nervous system; peripheral nervous system; idiopathic demyelinating polyneuropathy; Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia; chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis; granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity; inflammatory bowel disease; gluten-sensitive enteropathy; urticaria; Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis; psoriasis; atopic dermatitis; hypersensitivity pneumonitis; graft rejection; graft-versus-host disease.

OS Homo sapiens.

XX

PH Key Location/Qualifiers

PT Peptide 1..22 /label= Signal peptide

PT Modified-site 22..28 /label= N-myristoylation site

PT Protein 23..525 /label= Mature PRO4401

PT Modified-site 32..38 /label= N-myristoylation site

PT Modified-site 54..60 /label= N-myristoylation site

PT Modified-site 186..192 /label= N-myristoylation site

PT Modified-site 279..285 /label= N-myristoylation site

PT Modified-site 311..315 /label= N-myristoylation site

PT Modified-site 318..324 /label= N-myristoylation site

PT Domain 348..369 /label= Transmembrane domain

PT Modified-site 348..354 /label= N-myristoylation site

PT Modified-site 352..358 /label= N-myristoylation site

PT Modified-site 385..389 /label= N-myristoylation site

PT Modified-site 426..430 /label= CAMP + cGMP-dependant protein kinase

PT Modified-site 441..447 /label= N-myristylation site

PT Modified-site 453..457 /label= N-glycosylation site

FT Modified-site 475..479 /label= N-glycosylation site

FT Modified-site 479..483 /label= cAMP + cGMP-dependant protein kinase

FT phosphorylation site

XX

PR 07-JUN-2001.

XX

PR 10-NOV-2000; 2000WO-US030873.

XX

PR 30-NOV-1999; 99WO-US0203313.

PR 09-DEC-1999; 99US-0170262P.

PR 23-DEC-1999; 99US-0172059P.

PR 11-JAN-2000; 2000US-017581P.

PR 20-JAN-2000; 2000US-017718P.

PR 18-FEB-2000; 2000WO-US003342.

PR 03-MAR-2000; 2000WO-018702P.

PR 30-MAY-2000; 2000WO-US014941.

PR 05-JUN-2000; 2000US-020932P.

PR 24-AUG-2000; 2000WO-US023328.

XX

PA WO200140465-A2.

XX

PA (GETH) GENENTECH INC.

XX

PI Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL; Hillian KJ, Tumas D, Wattanabe CK, Wood WI, Zhang Z;

XX

DR WPI: 2001-381884/40.

XX

PT Isolated PRO polypeptide useful for treat or diagnose an immune-related disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis.

XX

PT Claim 1; Fig 12; 124pp; English.

CC The sequences given in AAB47291-99 show PRO polypeptides. PRO1081, PRO1274 and PRO10272 stimulate the proliferation of T-lymphocytes and PRO1199, PRO1556, PRO401 and PRO10268 inhibit the proliferation of T-lymphocytes. PRO1199 and PRO912 act to enhance the infiltration of mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN) into the tissue of a mammal. The PRO cDNA's and antibodies which bind to them, are used to treat an immune-related disorder in a mammal. Such disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, primary biliary cirrhosis, idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease.

CC Sequence 525 AA;

CC

Query Match Best Local Similarity 54.5%; Score 470; DB 4; Length 525; Matches 84; Conservative 29; Mismatches 38; Index 2; Gaps 1;

XX

QY 6 SVLHLI-VASLILHLSGATKKKGEMKQTSETQKVQGTWTRHAEGIFTSNPYPSKYP 63
 |||| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
 8 SVLKVLITLVVREGIAVAKQDGONIGIKHPTQAGGIWRTSNGCHFASPNYPSYP 67

DB

OY 64 PDRRCIVILEAKAPRQTCIYFDPKYSTPSWECKFDIEVRDGFSPILRGFCQNP 123

Db	6 8	PNKECYILEAPRQRIELTFDHEYIERSFCRDLEVRDGPGFSPIDRCGVKSP	127	PR 20-DEC-1999; 99WO-US030911. PR 20-DEC-1999; 99WO-US030999. PR 22-DEC-1999; 99WO-US030720. PR 30-DEC-1999; 99WO-US031243. PR 30-DEC-1999; 99WO-US031274. PR 05-JAN-2000; 2000WO-US00219. PR 06-JAN-2000; 2000WO-US00277. PR 11-FEB-2000; 2000WO-US003565. PR 18-FEB-2000; 2000WO-US00411. PR 18-FEB-2000; 2000WO-US004342. PR 22-FEB-2000; 2000WO-US004414. PR 24-FEB-2000; 2000WO-US004914. PR 24-FEB-2000; 2000WO-US005004. PR 01-MAR-2000; 2000WO-US005601. PR 02-MAR-2000; 2000WO-US005746. PR 02-MAR-2000; 2000WO-US005841. PR 10-MAR-2000; 2000WO-US006319. PR 15-MAR-2000; 2000WO-US06884. PR 20-MAR-2000; 2000WO-US00737. PR 21-MAR-2000; 2000WO-US007532. PR 30-MAR-2000; 2000WO-US08439. PR 17-MAY-2000; 2000WO-US013705. PR 22-MAY-2000; 2000WO-US014042. PR 30-MAY-2000; 2000WO-US014941. PR 02-JUN-2000; 2000WO-US015264. PR 28-JUL-2000; 2000WO-US020710. PR 11-AUG-2000; 2000WO-US022031. PR 23-AUG-2000; 2000WO-US023522. PR 24-AUG-2000; 2000WO-US023228. PR 08-NOV-2000; 2000WO-US030952. PR 10-NOV-2000; 2000WO-US030873. PR 01-DEC-2000; 2000WO-US032678. PR 20-DEC-2000; 2000US-00747259. PR 20-DEC-2000; 2000WO-US034956. PR 28-FEB-2001; 2001US-00794498. PR 28-FEB-2001; 2001WO-US005220. PR 01-MAR-2001; 2001WO-US006666. PR 09-MAR-2001; 2001US-00802706. PR 14-MAR-2001; 2001US-00803689. PR 22-MAR-2001; 2001US-00816744. PR 05-APR-2001; 2001US-00828366. PR 10-MAY-2001; 2001US-00854280. PR 10-MAY-2001; 2001US-00854280. PR 18-MAY-2001; 2001US-00860216. PR 25-MAY-2001; 2001US-00866028. PR 25-MAY-2001; 2001US-00866034. PR 25-MAY-2001; 2001WO-US01192. PR 01-JUN-2001; 2001US-00872035. PR 01-JUN-2001; 2001WO-US017800. PR 05-JUN-2001; 2001US-00874503. PR 14-JUN-2001; 2001US-00882636. PR 19-JUN-2001; 2001US-00886342. PR 20-JUN-2001; 2001WO-US019692. PR 21-JUN-2001; 2001US-00887879. PR 22-JUN-2001; 2001WO-US02016. PR 29-JUN-2001; 2001WO-US021066. PR 09-JUL-2001; 2001WO-US021735. PR 18-JUL-2001; 2001US-00908122. PR 06-AUG-2001; 2001US-00924419. PR 09-AUG-2001; 2001US-00927796. PR 15-AUG-2001; 2001US-00931836. PR 19-DEC-2001; 2001US-00028072.
Db	124	PVIKSSGRFWIKERFADGELESMSGARYNTP	156	PA (GERTH) GENENTECH INC.
Qy	128	PLIRSTGRFMWIKFSSDEELLEGFLGRAKYSP	160	PA Baker KP., Berestini M., Deforge L., Desnoyers L., Filvaroff E., Gao W., Gerritsen ME., Goddard A., Godowski PJ., Gurney AL., Sherwood S., Smith N., Stewart TA., Tumas D., Watanabe CK., Wood WI., Zhang Z.; DR WPT; 2003-341980/32.
Db	XX			DR N PSDB; ACD23909.
RESULT	13			XX
ID	ABO17672	standard; protein;	525 AA.	
ID	ABO17672			
AC	ABO17672;			
XX				
DT	26-AUG-2003	(first entry)		
DE	Novel human secreted and transmembrane protein PRO4401.			
XX				
KW	Human; secreted and transmembrane protein; PRO; antiinflammatory; antiarteriosclerotic; cardiot; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (tNF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; AIDS; cardiac injury; infertility; birth defect; premature aging; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.			
OS	Homo sapiens.			
XX				
PN	US2003032156-A1.			
XX				
PD	13-FEB-2003.			
XX				
PR	05-MAY-2002;	2002US-00140474.		
XX				
PR	31-MAR-1997;	97WO-US005230.		
PR	12-JUN-1998;	98WO-US012456.		
PR	14-JUL-1998;	98WO-US014552.		
PR	28-AUG-1998;	98WO-US017888.		
PR	14-SEP-1998;	98WO-US018824.		
PR	14-SEP-1998;	98WO-US019093.		
PR	14-SEP-1998;	98WO-US019094.		
PR	16-SEP-1998;	98WO-US019177.		
PR	17-SEP-1998;	98WO-US019437.		
PR	07-OCT-1998;	98WO-US021141.		
PR	29-OCT-1998;	98WO-US022291.		
PR	29-OCT-1998;	98WO-US022292.		
PR	20-NOV-1998;	98WO-US024555.		
PR	01-DEC-1998;	98WO-US02455.		
PR	05-JAN-1999;	99WO-US000106.		
PR	08-MAY-1999;	99WO-US005028.		
PR	10-MAR-1999;	99WO-US005190.		
PR	20-APR-1999;	99WO-US008615.		
PR	14-MAY-1999;	99WO-US010733.		
PR	03-JUN-1999;	99WO-US012252.		
PR	01-SEP-1999;	99WO-US020111.		
PR	08-SEP-1999;	99WO-US020294.		
PR	13-SEP-1999;	99WO-US02044.		
PR	15-SEP-1999;	99WO-US021547.		
PR	05-OCT-1999;	99WO-US02089.		
PR	29-NOV-1999;	99WO-US022824.		
PR	30-NOV-1999;	99WO-US028313.		
PR	01-DEC-1999;	99WO-US028409.		
PR	01-DEC-1999;	99WO-US028301.		
PR	02-DEC-1999;	99WO-US028634.		
PR	02-DEC-1999;	99WO-US028551.		
PR	02-DEC-1999;	99WO-US028564.		
PR	02-DEC-1999;	99WO-US028565.		
PR	16-DEC-1999;	99WO-US028565.		
PR	16-DEC-1999;	99WO-US030095.		

PT New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.

XX Claim 12; Fig 114; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a biactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIa, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The peptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

XX Sequence 525 AA;

	Query Match	Local Similarity	Score	DB	Length
Matches	84;	Conservative	54.9%	6;	525;
	84;	Mismatches	29;		
		Indels	38;		
		Gaps	2;		
			1;		

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QY 6 SVLHIT--VANILILHSAGAKKGTKQTISBTQKSVQCGTWKHEGGITSPNPKSP 63
Db 8 SVLKVLILTVLVEGIVAVAKTQDGTGQNGKHPATQCGWWRITSGHASPVPDSTP 67
QY 64 PDRECYTIAAPRCOELYDEKEVSIIESPWECKEDHIEVRDGPGRGFSPIGRQQGQNP 123
Db 68 PNKECTYILLAAPRQIETLDEHYXIEPPECRDHIEVRDGPGRGFSPIGLDRICGVKSP 127
QY 124 PVIKSSGRFWIKFFADGELESMGASARYVFTP 156
Db 128 PLIRSTGRFWIKFSSDEELIGLFRAKYSPIP 160

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RESULT 14

ID ABU80926 standard; protein; 525 AA.

XX ABU80926;

AC XX 23-JUN-2003 (first entry)

DE Human PRO polypeptide #57.

KW Human; PRO polypeptide; secreted and transmembrane protein; KW anti-PRO antibody; diagnostic assay; gene expression; diabetes; KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity; KW hearing loss; coagulation disorder; stroke; heart attack; cardiant; KW antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; KW antirheumatic; auditory; cerebroprotective; angiogenic.

XX Homo sapiens.

XX US2003004311-A1.

XX 02-JAN-2003.

XX

PR	19-DEC-2001; 2001US-00028072.
XX	18-JUN-1997; 97US-004911P.
PR	26-AUG-1997; 97US-005674P.
PR	17-SEP-1997; 97US-0059115P.
PR	17-SEP-1997; 97US-0059117P.
PR	17-SEP-1997; 97US-0059122P.
PR	17-SEP-1997; 97US-0059184P.
PR	18-SEP-1997; 97US-0059263P.
PR	19-SEP-1997; 97US-0059252P.
PR	19-SEP-1997; 97US-0059388P.
PR	24-SEP-1997; 97US-0059336P.
PR	17-OCT-1997; 97US-0062250P.
PR	17-OCT-1997; 97US-0062285P.
PR	17-OCT-1997; 97US-0062287P.
PR	17-OCT-1997; 97US-0063755P.
PR	24-OCT-1997; 97US-006214P.
PR	24-OCT-1997; 97US-0062816P.
PR	24-OCT-1997; 97US-006345P.
PR	24-OCT-1997; 97US-006382P.
PR	24-OCT-1997; 97US-0063127P.
PR	27-OCT-1997; 97US-006327P.
PR	27-OCT-1997; 97US-006329P.
PR	28-OCT-1997; 97US-0063550P.
PR	28-OCT-1997; 97US-0063561P.
PR	29-OCT-1997; 97US-006304P.
PR	29-OCT-1997; 97US-0063733P.
PR	29-OCT-1997; 97US-0063735P.
PR	03-NOV-1997; 97US-0063738P.
PR	03-NOV-1997; 97US-0064809P.
PR	12-NOV-1997; 97US-0063186P.
PR	17-NOV-1997; 97US-0055846P.
PR	21-NOV-1997; 97US-006354P.
PR	24-NOV-1997; 97US-0063453P.
PR	24-NOV-1997; 97US-006511P.
PR	24-NOV-1997; 97US-0065170P.
PR	11-DEC-1997; 97US-006212P.
PR	11-DEC-1997; 97US-0059278P.
PR	11-DEC-1997; 97US-005934P.
PR	16-DEC-1997; 97US-0063694P.
PR	23-JAN-1998; 98US-0073612P.
PR	09-FEB-1998; 98US-0074086P.
PR	09-FEB-1998; 98US-0074902P.
PR	12-MAR-1998; 98US-007791P.
PR	20-MAR-1998; 98US-0078910P.
PR	25-MAR-1998; 98US-0079294P.
PR	27-MAR-1998; 98US-017963P.
PR	27-MAR-1998; 98US-007928P.
PR	31-MAR-1998; 98US-0080165P.
PR	14-JUL-1998; 98US-0012455.
PR	14-JUL-1998; 98US-0014552.
PR	28-AUG-1998; 98US-001788B.
PR	10-SEP-1998; 98US-0018824.
PR	14-SEP-1998; 98US-0019093.
PR	14-SEP-1998; 98US-0019177.
PR	17-SEP-1998; 98US-0019437.
PR	07-OCT-1998; 98US-0021141.
PR	29-OCT-1998; 98US-0022991.
PR	29-OCT-1998; 98US-0022992.
PR	20-NOV-1998; 98US-0024855.
PR	01-DEC-1998; 98US-0025108.
PR	05-JAN-1999; 99US-0001016.
PR	08-MAR-1999; 99US-0005028.
PR	10-MAR-1999; 99US-0015190.
PR	14-APR-1999; 99US-0008615.
PR	14-MAY-1999; 99US-0010733.
PR	02-JUN-1999; 99US-0012252.
PR	01-SEP-1999; 99US-0020111.

PR	08-SEP-1999;	99WO-US200594.
PR	13-SEP-1999;	99WO-US200944.
PR	15-SEP-1999;	99WO-US21090.
PR	15-SEP-1999;	99WO-US21547.
PR	05-OCT-1999;	99WO-US03089.
PR	29-NOV-1999;	99WO-US028214.
PR	30-NOV-1999;	99WO-US028313.
PR	30-NOV-1999;	99WO-US038409.
PR	01-DEC-1999;	99WO-US028301.
PR	01-DEC-1999;	99WO-US028634.
PR	02-DEC-1999;	99WO-US038551.
PR	02-DEC-1999;	99WO-US028564.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030991.
PR	30-DEC-1999;	99WO-US031243.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000277.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	22-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	01-MAR-2000;	2000WO-US005601.
PR	02-MAR-2000;	2000WO-US005746.
PA	(GETH) GENENTECH INC.	XX
XX	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	DE Human PRO polypeptide #57.
PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	XX
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	AC ABU6626;
XX	WPI ; 2003-352836/33.	XX
DR	N-PSPDB; AC67050.	DT 23-MAY-2003 (first entry)
XX	Claim 12; Fig 114; 643pp; English.	XX
XX	The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU80870-ABU8114 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipdibentry.html	XX
SQ	Sequence 525 AA;	OS Homo sapiens.
Query	Match 54.5%; Score 470; DE 6; Length 525;	XX
Query	Best Local Similarity 54.9%; Pred. No. 8.8e-45; Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;	XX
Qy	6 SVKIIIT-VASLILHLGATKKGGTEKQTSETOKSVQGTWIKHAEGCGFTSPNPKSKP 63	PR US200505190.
Db	8 SVKIVLTLTVLUVREGIAVAKTQDGQNTGKHPATQGIVWRTSNGHFASPNYPDSPY 67	PR 99WO-US020594.
Qy	64 PDRRCIVYIIEAPRQCIELYDFECKSISPSWCKEDFLHFLVRDGFPGFSPITIGRCFGQNP 123	PR 99WO-US020294.
Db	68 PNKCIVIYLIEAPRQCIELYDFECKSISFECKFDHFLVRDGFPGFSPPLIDRYCGYKSP 127	PR 99WO-US021090.

PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005811.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUN-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022311.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030973.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-0079498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00823366.
 PR 10-MAY-2001; 2001US-00854200.
 PR 18-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-0086034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-0088342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00897879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US0321066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.

XX SQ Sequence 525 AA;

Query	Match	Score	DB	Length
Qy	Best Local Similarity	54.5%	470	525
Matches	84;	Pred.	8.8e-45;	
	Conservative	No.		
	29;	Mismatches	38;	
		Indels	2;	
		Gaps	1;	
Db	6 SVLHIV-VASLILHSGATKGKTERQTSETQKSQGTWTKHAGGIFTSPNYSKP	63		
Qy	8 SVLKVLITLVNEVGIAVAKHQDGGNGIGKHPAQCGTWRVTSNGHFFASPNYDSYP	67		
Db	64 PDRECYIIEAPROQELYDEKSYSTEPSNECKFDHIEVRDGPFQFSPTGRFCQONP	123		
Qy	68 PNKECTYLEAPRQEELTDEHYVIEPSRECFLERVDGPFQFSPLIDRYCCVSKP	127		
Db	124 PVKSGGRFLWIKFEDGELELSMGESARYNFTP	156		
Qy	128 PLIRSGIGRFMWMKFSDEELBEGLGFRAKYSFP	160		

Search completed: May 18, 2004, 18:22:24
 Job time : 60 secs

PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR NPTI; 2003-33204/31.
 DR N-PSDB; ACA03659.

PT New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.

XX
 XX
 PS Claim 12; Fig 114; 660PP; English.

CC The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO and CC polypeptides are secreted and transmembrane proteins. The PRO

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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:19:46 ; Search time 39 Seconds

Perfect score: 852 US-09-887-593A-2 (without alignments)
Sequence: 1 MHGRGSHVHIVASLILHLS..... ADGELPSMGFSARYNFTPGK 158

Scoring table: BLOSUM62 Gapct 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBBL 25;*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	851	98.7	533 4 Q8TDP5	Q8tdp5 homo sapien
2	843	97.8	533 4 Q8EW85	Q8ew85 homo sapien
3	818	94.9	533 11 Q8RA17	Q8ra17 mus musculus
4	818	94.9	533 11 Q8DX39	Q8dx39 mus musculus
5	814	94.4	533 11 Q8C4S3	Q8c4s3 mus musculus
6	802	93.0	156 4 Q8TDP4	Q8tdp4 homo sapien
7	690	80.0	4 Q8ND78	Q8nd78 homo sapien
8	494	57.3	466 11 Q8CCM2	Q8ccm2 mus musculus
9	470	54.5	525 4 Q8NC67	Q8nc67 homo sapien
11	465	53.9	444 11 Q8E4Q8	Q8e4q8 mus musculus
12	53.9	52.5 11 Q8BNJ6	Q8bnj6 mus musculus	
13	34.1	39.6 4 Q8nd51	Q8nd51 homo sapien	
14	26.0	30.2 321 5 Q61849	Q61849 caenorhabditis	
15	25.0	29.0 5 Q9VYCT	Q9vyct drosophila	
16	23.8.5	27.7 11 Q62381	Q62381 mus musculus	

RESULT 1		ID	Q8TDP5	PRELIMINARY:	PRT:	533 AA.
AC		Q8TDP5;				
DT		01-JUN-2002	(TREMBLrel. 21, Created)			
DT		01-JUN-2002	(TREMBLrel. 21, Last sequence update)			
DE		01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
OS		Homo sapiens (Human).				
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX		NCBI_TaxID=9606;				
RN		[1]				
RP		SEQUENCE FROM N.A.				
RC		TISSUE:Retina;				
RX		MEDLINE:21940629; PubMed=11943477;				
RA		Stohr H., Berger C., Frohlich S., Weber B.H.;				
RT		"A novel gene encoding a putative transmembrane protein with two extracellular CUB domains and a low-density lipoprotein class A module: isolation of alternatively spliced isoforms in retina and brain."				
RT		Gene 28(223-231)(2002);				
RT		!- SIMILARITY: CONTAINS 2 CUB DOMAINS.				
RT		EMBL; AF448338; AAM18026.1; -.				
RT		GENBANK; HGNC:13823; NETO1.				
RT		InterPro: IPR000859; CUB.				
RT		InterPro: IPR002172; LDL_receptor_A.				
RT		PFAM; PF00431; CUB; 2.				
RT		PFAM; PR0057; LDL_recept_a; 1.				
RT		SMART; SM00442; CUB; 2.				
RT		SMART; SM0192; LDLa; 1.				
RT		PROSITE; PS01180; CUB; 2.				
RT		PROSITE; PS0068; LDLa; 2; 1.				
SQ		SEQUENCE: 533 AA; 60218 MW; 5B3EB7BBB8031BL CRC64;				
Query Match		98.7%; Score 851; DB 4; Length 533;				
Best Local Similarity		100.0%; Pred. No. 1.1e-85;				
Matches		156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

[2] SEQUENCE FROM N.A.
Tissue: Brain;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN [3] SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12810072;
RA Michishita M., Ikeda T., Nakashiba T., Ogawa M., Tashiro K., Honjo T.,
RA Doi K., Itohara S., Endo S.;
RT "A novel gene, Btcl, encoding CUB and LDLa domains is expressed in
RT restricted areas of mouse brain.";
RL Biochem. Biophys. Res. Commun. 306:680-686 (2003).
DR BCO5145; AANH5145; -;
EMBL; AV138990; AAN38318.1; -;
DR InterPro; IPR000859; CUB.
DR InterPro; IPR002172; LDL_receptor_A.
DR Pfam; PF00431; CUB; 2.
DR SMART; SMO0192; LDLa; 1.
DR SMART; SMO0042; CUB; 2.
DR SMART; SMO0192; LDLa; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00068; LDLRa_2; 1.
KW transmembrane.
SQ Sequence 533 AA; 60242 MW; 6375B395421D558F CRC64;
Query Match 94.9%; Score 818; DB 11; Length 533;
Best Local Similarity 94.2%; Pred. No. 4.9e-82;
Matches 147; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 MTHGRSVVHIVASILIHLSGATKGKTKQTSETQKSVQCGTWTHAEGGIFTSPNPNPS 60
1 MTHGRSLPHIHLASILIHLSGATKGKTKQTSETQKSVQCGTWTHAEGGIFTSPNPNPS 60
Db 1 MTHGRSLRHITASLILIHLSGATKGKTKQTSETQKSVQCGTWTHAEGGIFTSPNPNPS 60
QY 61 KYPDPRECTYIIEAAPROCYIELFDEKSIIESPWECKDHIERDGPFGSPIGRQQ 120
61 KYPDPRECTYIIEAAPROCYIELFDEKSIIESPWECKDHIERDGPFGSPIGRQQ 120
Db 61 KYPDPRECTYIIEAAPROCYIELFDEKSIIESPWECKDHIERDGPFGSPIGRQQ 120
QY 121 QNPPIVKSSGRFLWIKFFADGELESMGFSARVNFTP 156
121 QNPPIVKSSGRFLWIKFFADGELESMGFSARVNFTP 156
Db 121 QNPPIVKSSGRFLWIKFFADGELESMGFSARVNFTP 156
RESULT 5
QB4S3 PRELIMINARY; PRT; 533 AA.
ID QPC4S3 PRELIMINARY; PRT; 156 AA.
AC QPC4S3;
DT 01-MAR-2003 (Tremblel. 23, Created)
DT 01-MAR-2003 (Tremblel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblel. 25, Last annotation update)
DE Hypothetical Microbodies C-terminal targeting signal/LDL-receptor
DR Class A.
GN NEU01.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=2234683; PubMed=12466851;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.;
RL Nature 420:563-573 (2002).
DR EMBL; AK081325; BAC38196.1; -.
DR MGI:2180216; Neto1.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR002172; LDL_receptor_A.

RESULT 7

O8ND78 PRELIMINARY; PRT; 500 AA.

ID Q8ND78;

AC 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DR 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RP TISSUE=Brain; Ansborge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.; DR EMBL; ALB4354; CAD9019.1; -.

RA Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.

DR InterPro: IPR000859; CUB.

DR InterPro: IPR02172; LDL_receptor_A.

DR Pfam: PF00431; CUB; 2.

DR Pfam: PF00431; LDL_recept_a; 1.

DR SMART; SMART_00042; CUB; 2.

DR PROSITE; PS00192; LDL; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS50068; LDLRA_2; 1.

DR PROSITE; PS50068; LDLRA_2; 1.

DR SMART; SMART_00042; CUB; 2.

DR PROSITE; PS00192; LDL; 1.

DR PROSITE; PS01180; CUB; 2.

DR Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 466 AA; 52840 MW; FE4AEAA037EB34D9 CRC64;

Query Match 57.3%; Score 494; DB 11; Length 466; Best Local Similarity 98.9%; Pred. No. 3.8e-06; Indels 0; Gaps 0; Matches 88; Conservative 1; Mismatches 0;

QY 68 CIVYIIRAPROCIELYFDKYSIERPWECKTDHIEVRDGPGRSPTRIGRCGQONPVIK 127

Db 1 CVYIIRAPROCIELYFDKYSIESPWECKFDHIEVRDGPGRSPTRIGRCGQONPVIK 60

Qy 128 SSGREFLWIKFADGELESMGISARVNPTP 156

Db 61 SSGREFLWIKFADGELESMGISARVNPTP 89

Qy 34 ETQKSYVCGTMWKHAGGIFTSPNPKYKPPRECYIEAARPROCIELYFDKYSIERS 93

Db 1 ETOKSYVCGTWTWKHAGGIFTSPNPKYKPPRECYIEAARPROCIELYFDKYSIERS 60

QY 94 WECKFDHEIVRDGPFGFSPPIGRFCGQONPVIKSSGRFLMKFFADGELESMGISARYN 153

Db 61 WECKFDHEIVRDGPFGFSPPIGRFCGQONPVIKSSGRFLMKFFADGELESMGISARYN 120

QY 154 FPP 156

Db 121 FPP 123

RESULT 8

O8CCM2 PRELIMINARY; PRT; 466 AA.

ID O8CCM2;

AC 01-MAR-2003 (T-EMBLrel. 23, Created)

DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical Microbodies C-terminal targeting signal/LDL-receptor DE Class A (Fragment).

GN NETO1.

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Olfactory brain;

RC MEDLINE=22354683; PubMed=12466851;

RA THE FANTOM Consortium,

RA "Analysis of the mouse transcriptome based on functional annotation of RT RT full-length cDNAs.",

RT Nature 420:563-573 (2002).

RL EMBL; AK032510; BAC27902.1; -.

Query Match 54.5%; Score 470; DB 4; Length 525; Best Local Similarity 54.9%; Pred. No. 2e-43; Indels 2; Gaps 1; Matches 84; Conservative 29; Mismatches 38;

Qy 6 SVLHI--VASLILHLSGATKGKGTEQQTSTTQKSVQCGWTKAEGGIFTSPNPKYF 63

Db 8 SVLKVLITLVLEVGIAVQAQKQDGQNGIKRIPATQGIGWRTSNGHASPNVYDPS 67

Qy 64 PDIRECTTYIEAARPROCIELYFDKYSIERSWCKFDHEIVRDGPFGFSPTRIGRCGQONPVIK 123

Db 68 PNKECYIILEMAPQRQIETDFEHTYIEPSFCRFDHIEVRDGPFGFSPPLIDRYCIGKSP 127

OY	124	PVIKSSGRLEWIKFADGELESMGFSARVNFTP	156	DR PROSIM; P55006B; IDURA_2; 1.
ID	072381	PRELIMINARY;	PRT;	491 AA.
AC	Q72381;			
DT	01-OCT-2003	(TREMBirel. 25, Created)		
DT	01-OCT-2003	(TREMBirel. 25, Last sequence update)		
DT	01-OCT-2003	(TREMBirel. 25, Last annotation update)		
DE	Hypothetical protein DKFZP086N1919B (Fragment).			
GN	DKFZP086N1919B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Human fetal brain;			
RA	Bloesser H., Boehler M., Mewes H.W., Weil B., Amid C., Osanger A.,			
RA	Fobo G., Han M., Wiedemann S.; EMBL/GenBank/DBJ/ databases.			
DR	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
KW	Hypothetical protein.			
FT	NON_TER			
SQ	NON_TER 1			
SEQUENCE	491 AA;	55641 MW;	3608CFA37BE1C6AC	CRC64;
Query Match	54.3%	Score 468;	DB 4;	Length 491;
Best Local Similarity	53.7%	Pred. No. 6e-43;	Indels 20;	Gaps 0;
Matches	78;	Conservative	21;	Mismatches 0;
Score	65.5%	Pred. No. 3.1e-43;	Indels 0;	Gaps 0;
QY	38	SVQCGGTWTKAEGGIFTSPVPSKPPDRCIYIKAAPQCIELYDEKYSIESWEEK	97	
Db	8	ATQCGGIWVTRNSNGHFASPVYDSDYSPNPKCIVYLEAPQRQIELTDEEYVIPSFCT	67	
QY	98	FDHIEVRDGPGFSITIGRQGQONPPVKSGLRFWIKETFADGELESMGFSARVNFTP	156	
Db	68	FDHIEVRDGPGFSPLIDRYCGVKSPPLIRSTGRPMWIKESSDELEGIGFRAKSFIP	126	
RESULT	11			
Q8CAQ8				
PRELIMINARY;				
PRT;	444 AA.			
AC	Q8CAQ8;			
DT	01-MAR-2003	(TREMBirel. 23, Created)		
DT	01-OCT-2003	(TREMBirel. 23, Last sequence update)		
DT	01-OCT-2003	(TREMBirel. 25, Last annotation update)		
DE	Hypothetical LDL-receptor class A (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TAXID=10990;			
RA	The RIKEN Genom Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs";			
RT	Nature 420:563-573 (2002).			
DR	EMBL; AK038512; BAC38998; 1, -.			
DR	MGI; MGI:1921763; Neto2.			
DR	InterPro; IPRO00059; CUB.			
DR	InterPro; IPRO20172; LDL_receptor_A.			
DR	Pfam; PF00431; CUB; 2.			
DR	SMART; SM0042; CUB; 2.			
DR	SMART; SM00192; IDRA; 1.			
DR	PROSITE; PS01180; CUB; 2.			
DR	PROSITE; PS00068; IDRA_2; 1.			
KW	Hypothetical protein.			
SQ	SEQUENCE 525 AA;			
Query Match	53.9%	Score 465;	DB 11;	Length 525;
Best Local Similarity	53.7%	Pred. No. 7.3e-43;	Indels 31;	Gaps 0;
Matches	79;	Conservative	31;	Mismatches 31;
Score	65.5%	Pred. No. 3.1e-43;	Indels 0;	Gaps 0;
QY	10	IVASLITHLHSGATKKGGTQEQTSETQKSVQCGTWTHAEGGIFTSPVPSKPPDRCI	69	
Db	14	LITLVVVEGIAVAKQTODGQNGIGKHPATQOGIWTNSNGHFASPVYDSDYSPNPNECI	73	
QY	70	YIKAAPQCIELYDEKYSIESWEEKFDHIEVRDGPGFSPLIDRYCGVKSPPLIRST	129	
Db	74	YIKAAPQCIELYDEKYSIESWEEKFDHIEVRDGPGFSPLIDRYCGVKSPPLIRST	133	
QY	130	GRFLWIKFFADGELESMGFSARVNFTP	156	
Db	134	GRFLWIKFFADGELESMGFSARVNFTP	160	

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Thegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft J., Kravitz S., Kulp D., Lai Z.,
 RA Iasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matthei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkukov G., Milshina N.V., Mobarry C., Morris J., Moskrefi A.,
 RA Mount R.M., Moy M., Murphy B., Murphy D.M., Nelson D.M., Nelson D.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Pelizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svartkas R., Tector C., Turner R., Venter C., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Yee J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celinkker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanaiides P.G., Brandao R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Carlson J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Douc L.E., Doyle C., Dresneak D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moskrefi A.,
 RA McIntosh T.C., Moy M., Murphy D., Nelson K.A., Nunoo J.,
 RA Paclob J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svartkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RL "Sequencing of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Bradeczyk P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinkker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whittlefield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinkker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FLYbase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Chapman M., Brockstein P., Hong L., Agbayani A., Carlson J.,
 RA Chapman M., Brockstein P., Hong L., Agbayani A., Carlson J.,
 RA George R., Gonzalez M., Guarini H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Paclob J., Paragas V., Park S.,
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinkker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 CC -- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL; AE003492; AAF49276.2; -
 DR EMBL; AY070839; AAL48461.1; -
 DR FLYBase; FGEN0052635; CG33635.
 DR InterPro; IPR008859; CUB.
 DR InterPro; IPR021727; LDL-receptor_A.
 DR Pfam; PF00331; CUB; 2.
 DR Pfam; PF00331; CUB; 2.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:16:31 ; Search time 17 Seconds

Sequence: US-09-887-593A-2
 Perfect score: 862
 Sequence: 1 MIHGRSVLHVAVASLILHLS.....ADGELESMGFSARYNFTPGK 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 & Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	232.5	27.0	914	1 NRPL CHICK P79795 gallus gallus
2	227	26.3	707	1 BNP1_XENLA P98070 xenopus laevis
3	226	26.1	931	1 NRPL_MOUSE P35375 mus musculus
4	225	26.1	925	1 NRPL_RAT P35276 rattus norvegicus
5	224	26.0	931	1 NRPL_HUMAN P60452 homo sapiens
6	224	25.6	991	1 BNP1_MOUSE P98053 mus musculus
7	221	25.6	923	1 NRPL_HUMAN O14736 homo sapiens
8	220.5	25.6	986	1 BNP1_HUMAN P13497 homo sapiens
9	217.5	25.6	1022	1 TUD_BRAE P57460 brachydanio P25733 drosophila
10	217.5	25.2	1057	1 TUD_DROME P25733 drosophila
11	217	25.2	922	1 NRPL_RAT Q9WQ99 rattus norvegicus
12	215	25.1	923	1 NRPL_MOUSE P97533 mus musculus
13	215	24.9	639	1 BNP1_STRPV P98049 stronglylobo Q15113 homo sapiens
14	201.5	23.4	449	1 PCO1_HUMAN P28824 xenopus laevis
15	198.5	23.0	928	1 NRPL_XENLA Q61398 mus musculus
16	194.5	22.6	468	1 PCO1_MOUSE Q08638 rattus norvegicus
17	194.5	22.6	468	1 PCO1_RAT Q08638 rattus norvegicus
18	21.6	21.6	3564	1 CSM1_MOUSE Q92119 mus musculus
19	184.5	21.4	3565	1 CSM1_HUMAN Q96P77 homo sapiens
20	182	21.1	3487	1 CSM2_HUMAN Q7Z408 homo sapiens
21	178.5	20.7	699	1 CRAB_HUMAN P48740 h. complementum P42674 paracentrotrotula
22	173.5	20.1	597	1 RP10_PARLI P08079 mus musculus
23	163.5	19.0	2796	1 CSM3_MOUSE Q7Z407 homo sapiens
24	163.5	19.0	1	1 CRAB_MOUSE P98064 mus musculus
25	162.5	18.9	704	1 ST14_HUMAN Q9Y661 homo sapiens
26	161.5	18.7	859	1 ST14_HUMAN P98068 stronglylobo
27	160.5	18.6	1	1 SPAN_STRPU P00736 homo sapiens
28	152.5	17.7	705	1 CIR_HUMAN Q08059 mus musculus
29	151	17.5	1	1 TSG6_MOUSE P98066 homo sapiens
30	151	17.5	277	1 HUMAN P46622 cocturnix coquelinii
31	150	17.4	310	1 ASTL_COQJA P98065 homo sapiens
32	149.5	17.3	855	1 ST14_HUMAN Q9Y566 homo sapiens
33	148	17.2	1	1 TSG6_RABIT P98065 oryzolagrus

US-09-887-593A-2
 (without alignments)
 483.946 Million cell updates/sec

US-09-887-593A-2
 (without alignments)
 483.946 Million cell updates/sec

ALIGNMENTS

RESULT 1
 NRPL_CHICK STANDARD; PRT; 914 AA.
 ID NRPL_CHICK
 AC P79795;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 41, Last annotation update)
 DE Neuropilin-1 precursor (As protein).
 GN NRPL OR NRPL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galloformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN NCBI_TAXID=9031;

[1] -
 SEQUENCE FROM N.A.
 STRAIN=White Leghorn; TISSUE=Embryonic brain;
 RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A., Fujikawa H.;
 RA "Expression of a cell adhesion molecule, neuropilin, in the developing chick nervous system.";
 RT Dev. Biol. 170:207-222(1995).
 RL CC
 CC FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neural circuits and in organogenesis outside the nervous system. It mediates the chemorepulsive activity of semaphorins (By similarity). Seems to have calcium-independent cell adhesion properties.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- TISSUE SPECIFICITY: Developing nervous system; optic tectum (layers D and E of GTS), amacrine cells of retina, neurites of dorsal root ganglia. Also expressed in nonneuronal cells, e.g. blood vessel in the entire embryo.
 CC -|- SIMILARITY: Belongs to the neuropilin family.
 CC -|- SIMILARITY: Contains 2 CUB domains.
 CC -|- SIMILARITY: Contains 2 F5/F8 type C domains.
 CC -|- SIMILARITY: Contains 1 MM domain.

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EMBL; D5416; BAA8256.1; -;
 HSSP; PI2259; ICZT;
 InterPro; IPR00859; CUB.
 InterPro; IPR00421; FAB_C.
 InterPro; IPR008979; Galbind like.
 InterPro; IPR00898; MM_domain.
 Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 Pfam; PF00629; MM; 1.

DR PRINTS; PRO0022; MANDOMAIN.
 DR SMART; SM0042; CUB; 2.
 DR SMART; SM0023; FA58C; 2.
 DR SMART; SM0137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01286; FA58C_1; 2.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
 Recptor; Cell adhesion.
 FT SIGNAL 1 18 POTENTIAL.
 FT DOMAIN 1 9 NEUROPILIN-1.
 FT DOMAIN 20 870 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 848 POTENTIAL.
 FT DOMAIN 871 914 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 139 CUB 1.
 FT DOMAIN 145 263 CUB 2.
 FT DOMAIN 273 422 F5_8 TYPE C 1.
 FT DOMAIN 429 801 F5_8 TYPE C 2.
 FT DOMAIN 636 801 MAM.
 FT DISULFID 25 52 PROBABLE.
 FT DISULFID 80 102 PROBABLE.
 FT DISULFID 145 171 PROBABLE.
 FT DISULFID 204 226 PROBABLE.
 FT DISULFID 273 422 BY SIMILARITY.
 FT DISULFID 429 581 BY SIMILARITY.
 SQ SEQUENCE 914 AA; 102480 MW; DD2EE6D6FOCB6BC CRC64;

Query Match 27.0%; Score 232.5; DB 1; Length 914;
 Best Local Similarity 35.3%; Pred. No. 4e-16; 55; Indels 19; Gaps 4;
 Matches 54; Conservative 25; Mismatches 16; 55; Signal 1.

QY 15 IIITHLSGATKKGTEKKQTSETOKSVQCGWTKHAGGIFTSPNYPNSKCPDRECTYIEA 74
 Db 5 LFFHCAAIT----FTISRALSDKCGDTIKLISPGVITSPGPYQFQPSQHSQCKEWLQA 58
 QY 75 -APRQCILEYDFEKYSIERSWEEKFDHIEVRDPFGFSPILIGRGQONPPVKGSGREL 133
 Db 5.9 PEPYQRIMINFNPHFDLED-RDKDYVEVIDGNNAEGRILWKGKYCGKLAAPPLVSSGPYL 117
 QY 134 WIKFFPDAEGELEMGSFQFARY-----NFT 155
 Db 118 FIKEVSDYETHGAGFSIRVEVKRGPGECRSRNFT 150

RESULT 2

ENZYME	XENLA	STANDARD;	PRT;	707 AA.
ID	BMP1_XENLA			
AC	P98070;			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OB	NCBI_TAXID:8335;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
CC	MEDLINE=9405787; PubMed=8262384;			
CC	Maeno M., Xue Y., Wood T.I., Ong R.C./, Kung H.F./			
CC	"Cloning and expression of cDNA encoding <i>Xenopus laevis</i> bone morphogenic protein-1 during early embryonic development.",			
CC	- - DEVELOPMENTAL STAGE: Blastula, early gastrula and hatched tadpoles; little or no expression in morula and late gastrula.			
CC	- - SIMILARITY: Belongs to peptidase family M12A.			

FT SIGNAL 1 18 POTENTIAL.
 FT DOMAIN 20 870 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 848 POTENTIAL.
 FT DOMAIN 871 914 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 139 CUB 1.
 FT DOMAIN 145 263 CUB 2.
 FT DOMAIN 273 422 F5_8 TYPE C 1.
 FT DOMAIN 429 801 F5_8 TYPE C 2.
 FT DOMAIN 636 801 MAM.
 FT DISULFID 25 52 PROBABLE.
 FT DISULFID 80 102 PROBABLE.
 FT DISULFID 145 171 PROBABLE.
 FT DISULFID 204 226 PROBABLE.
 FT DISULFID 273 422 BY SIMILARITY.
 FT DISULFID 429 581 BY SIMILARITY.
 SQ SEQUENCE 914 AA; 102480 MW; DD2EE6D6FOCB6BC CRC64;

Query Match 26.3%; Score 227; DB 1; Length 707;
 Best Local Similarity 40.2%; Pred. No. 1e-15; 45; Indels 2; Gaps 2;
 Matches 45; Conservative 18; Mismatches 47; Signal 1.

QY 41 OCTWTKHAEG3FTSPNYPSKCPDRECTYIEAAPRQCILEYDFEKYSIERSWEEKFDH 100
 Db 398 CGEVVKKDSGH1-OSPNYDPDRPKACWVKUSVSEGPHVGISF-QSFBIERHDSCAVD 455
 QY 101 IEVDGPGFSTIGRGQONPPVKGSGRELWIKFFADGELEMGSFARY 152
 Db 456 LEIRDGSESETSPLVGRGCGYKEDDIDKSTNQIWKIFVSDGSINKAGFSINY 507

Db	141	IFKTGSEDCSKNFT	154
ID	NRP2_RAT	STANDARD;	PRT; 925 AA.
RESULT	4		
AC	035776;	O35776;	16-OCT-2001 (Rel. 40, Created)
DT			16-OCT-2001 (Rel. 40, Last sequence update)
DT			15-MAR-2004 (Rel. 43, last annotation update)
DE	Neuropilin-2 precursor (vascular endothelial cell growth factor 165 receptor 2).		
GN	GNP2.		
OS	Rattus norvegicus (Rat).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]	SEQUENCE FROM N.A.	
RC	STRAIN=Sprague-Dawley;		
RX	MLINE=97433085; PubMed=9288754;		
RA	Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,		
RA	Giny D.D.,	"Neuropilin is a semaphorin III receptor.",	
RL	Cell 90:753-762(1997).		
CC	-!- FUNCTION: High affinity receptor for semaphorins 3C, 3F' VEGF-165 and VEGF-145 isoforms of PEGF, and the PLGF-2 isoform of PEGF.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- TISSUE SPECIFICITY: Found in certain neuronal populations of the CNS and in other nonneuronal tissues including mesenchymal tissue lining in the ribs.		
CC	-!- SIMILARITY: Belongs to the neuropilin family.		
CC	-!- SIMILARITY: Contains 2 CUB domains.		
CC	-!- SIMILARITY: Contains 1 MAM domain.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; AF016297; AAC53338.1; .		
DR	EMSP; P12259; ICZI.		
DR	InterPro; IPR000859; CUB.		
DR	InterPro; IPR000998; MAM_C.		
DR	InterPro; IPR00421; PAFB_C.		
DR	PFam; PF00331; CUB.		
DR	PFam; PF00754; F5_F8_type_C; 2.		
DR	PFam; PF0029; MAM_1.		
DR	PRINTS; PR0020; MAMOMAIN.		
DR	SMART; SM0042; CUB; 2.		
DR	SMART; SM00231; PAFBC; 2.		
DR	SMART; SM00137; MAM; 1.		
DR	PROSITE; PS01180; CUB; 2.		
DR	PROSITE; PS01285; FAB8C_1; 2.		
DR	PROSITE; PS01286; FAB8C_2; 2.		
DR	PROSITE; PS50022; FAB8C_3; 2.		
DR	PROSITE; PS50060; MAM_2; 1.		
KW	Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.		
FT	SIGNAL 1	POTENTIAL.	
FT	CHAIN 23	925 NEUROPILIN-2.	
FT	DOMAIN 23	858 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 859	883 POTENTIAL.	
FT	DOMAIN 884	925 CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN 28	142 CUB 1.	
FT	DOMAIN 149	267 CUB 2.	
FT	DOMAIN 277	427 F5/8 TYPE C 1.	
FT	DOMAIN 434	592 F5/8 TYPE C 2.	
FT	DOMAIN 642	802 MAM.	
RP	CHARACTERIZATION		
RP	MLINE=20309748; PubMed=10748121;		
RA	Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G., Klagsbrun M.; Soker S., Takashima S., Mao H.-Q., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.", Cell 92:735-745(1998).		
RR	(3)		
RR	CHARACTERIZATION		
RR	MLINE=20309748; PubMed=10748121;		
RA	Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G., Klagsbrun M.; Soker S., Takashima S., Mao H.-Q., Neufeld G., Klagsbrun M.; "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placent growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.", J. Biol. Chem. 275:18040-18045(2000).		
CC	-!- FUNCTION: High affinity receptor for semaphorins 3C, 3F' VEGF-165 and VEGF-145 isoforms of PEGF, and the PLGF-2 isoform of PEGF.		
CC	-!- SUBUNIT: Neuropilin-2 probably forms an heteromeric complex with neuropilin-1 in order to be a functional semaphorin 3C receptor.		
FT	DISULPID	28	55 BY SIMILARITY.
FT	DISULPID	83	105 BY SIMILARITY.
FT	DISULPID	149	175 BY SIMILARITY.
FT	DISULPID	208	230 BY SIMILARITY.
FT	DISULPID	277	427 BY SIMILARITY.
FT	CARBONYD	434	592 BY SIMILARITY.
FT	CARBONYD	152	152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD	157	157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD	629	629 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD	833	833 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD	834	834 N-LINKED (GLCNAC. .) (POTENTIAL).
SO	SEQUENCE	925 AA;	10896 MN; 3BF62903F643851C CRC64;
Db	Query Match	26.1%	Score 225; DB 1; Length 925;
Db	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
Db	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93	
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
QY	153 -----NPT 155		
Db	141	IFKTGSEDCSKNFT	154
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-	152	
Db	81 HDCKDPFIERTDGDSEBSADLIGKHCNTAAPTISGSVXIKFSDYARQAGASLRYE	140	
RR	Query Match	26.1%	Score 225; DB 1; Length 925;
RR	Local Similarity	37.3%	Pred. No. 2.4e-15; Gaps 3;
RR	Matches	50;	Conservative 19; Mismatches 51; Indels 14;
RR	Indels	14;	Gaps 3;
RR	QY	35 TOKSYQCGTMKHAARGGIFTSPNYRSKPPRECIVYIENA-APROCIELYDFEKYSIEPS	93
Db	32 SQQDPGCGRNLNSKDAAGYITSPGYFQDYPHQNCEWWVVAPEPNQKIVLNPNPHREIE-K	80	
QY	94 WECKFDHETRDGPFGPSPIIGRFQONPVKSGRFRWIKFPRADGEWSMGSRAY-		

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=A22;
 CC IsoId:060462-1; Sequence=Displayed;
 CC
 CC Name=A0;
 CC IsoId:060462-2; Sequence=vsp_004342;
 CC
 CC Name=A17;
 CC IsoId:060462-3; Sequence=vsp_004341;
 CC
 CC -!- SIMILARITY: Belongs to the neuropilin family.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -!- SIMILARITY: Contains 1 MAM domain.
 CC
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 DR EMBL; AF022859; AAC51788.1; --.
 DR EMBL; AF022860; AAC51789.1; --.
 DR EMBL; AF016098; AAC12922.1; --.
 DR HSSP; P12259; ICUT.
 DR Genew; HGNC; 8005; NRP2.
 DR MM; 602070; --.
 DR GO; GO:005624; C:membrane fraction; TAS.
 DR GO; GO:000872; F:receptor activity; TAS.
 DR GO; GO:005021; F:vascular endothelial growth factor receptor . . ; TAS.
 DR GO; GO:000411; P:axon guidance; TAS.
 DR InterPro; IPR00859; CUB.
 DR InterPro; IPR00421; F458_C.
 DR InterPro; IPR00879; Gal_Bind like.
 DR InterPro; IPR00998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_F8_TYPE_C; 2.
 DR Prints; PRO0020; MAM_DOMAIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FA58C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FA58C; 1; 2.
 DR PROSITE; PS01286; FA58C; 2; 2.
 DR PROSITE; PS00022; FAS8C; 3; 2.
 DR PROSITE; PS50060; MAM_2; 1.
 KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
 KW Alternative splicing.
 FT SIGNAL 1 20 OR 22 (POTENTIAL).
 FT CHAIN 21 931 NEUROPILIN-2.
 FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 865 889 POTENTIAL.
 FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 142 CUB 1.
 FT DOMAIN 149 267 CUB 2.
 FT DOMAIN 277 427 F5/8 TYPE C 1.
 FT DOMAIN 434 592 F5/8 TYPE C 2.
 FT DOMAIN 642 802 MAM.
 FT DOMAIN 671 674 POLY-SER.
 FT DISUFID 28 55 BY SIMILARITY.
 FT DISUFID 83 105 BY SIMILARITY.
 FT DISUFID 149 175 BY SIMILARITY.
 FT DISUFID 208 230 BY SIMILARITY.
 FT DISUFID 277 427 BY SIMILARITY.
 FT DISUFID 434 592 BY SIMILARITY.
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 839 839 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 809 813 Missing (in isoform A17).
 /FTid=vsp_004341.
 CC
 CC RESULT 6
 CC BMP1_MOUSE
 ID BMP1_MOUSE STANDARD PRT 991 AA.
 AC P98063;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE Bone morphogenetic protein 1 precursor (BC 3.4.24.19) (BMP-1)
 DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mrr1d).
 GN BMP1.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10909;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6; TISSUE=Embryo;
 RX MEDLINE=94222342; PubMed=8147472;
 RA Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
 RT "embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
 RT which is related to the Drosophila tolloid gene tolloid and
 RT encodes a putative astacin metalloendopeptidase.";
 RL Dev. Biol. 163:175-183(1994).
 CC -!- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
 CC and III. Induces cartilage and bone formation.
 CC -!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
 CC Ala-|-[Asp in type I and II procollagens and at Arg-|-[Asp in type
 CC III.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- ENZYME REGULATION: Activity is increased by the procollagen C-
 CC endopeptidase enhancer protein.
 CC -!- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
 CC and floor plate region of the neural tube. Less in developing
 CC membranous and endochondral bone, submucosa of intestine, dermis
 CC of skin and the mesenchyme of spleen and lung.
 CC -!- SIMILARITY: Belongs to peptidase family M12A.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 5 CUB domains.
 CC
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 CC
 DR EMBL; I24755; AA337306.1; --.
 DR PIR; I49540; I49540.
 DR HSSP; P00736; IAPQ.
 DR MRSPS; ML2_005; --.
 DR

DR	MGD; MGI:88176; Bmp1.	Db	855 KGFQASHS 862
DR	InterPro; IPR00152; Asx_hydroxyl_S.		
DR	InterPro; IPR00085; CUB.		
DR	InterPro; IPR00188; EGF_Ca.		
DR	InterPro; IPR006209; EGF_Like.		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		
DR	InterPro; IPR006026; Peptidase_M.		
DR	InterPro; IPR001506; Peptidase_M12A.		
DR	Pfam; PF00431; CUB; 5.		
DR	Pfam; PF00008; EGF; 2.		
DR	PRINTS; PR00480; ASPCIN.		
DR	SMART; SMC0042; CUB; 5.		
DR	SMART; SMC0179; EGF_Ca; 2.		
DR	FROSTIE; PS00010; ASX_HYDROXYL; 2.		
DR	FROSTIE; PS00180; CUB; 5.		
DR	FROSTIE; PS00182; EGF; 1; FALSE_NEG.		
DR	FROSTIE; PS00186; EGF; 2; 2.		
DR	FROSTIE; PS00142; ZINC_PROTEASE; 1.		
KW	Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;		
KW	Hydrolase; Metalloprotease; Zinc-like domain; Zinc; Calcium; Signal;		
KW	Glycoprotein; Zymogen.		
FT	SIGNAL	2	POTENTIAL.
FT	PROPE	25	POTENTIAL.
FT	CHAIN	126	BONE MORPHOGENETIC PROTEIN 1.
FT	DOMAIN	126	METALLOPROTEASE.
FT	DOMAIN	327	CUB 1.
FT	DOMAIN	440	CUB 2.
FT	DOMAIN	552	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	593	CUB 3.
FT	DOMAIN	708	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	752	CUB 4.
FT	DOMAIN	865	CUB 5.
FT	METAL	218	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	219	BY SIMILARITY.
FT	METAL	222	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	228	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISULPID	188	BY SIMILARITY.
FT	DISULPID	327	BY SIMILARITY.
FT	DISULPID	380	BY SIMILARITY.
FT	DISULPID	440	BY SIMILARITY.
FT	DISULPID	466	BY SIMILARITY.
FT	DISULPID	493	BY SIMILARITY.
FT	DISULPID	515	BY SIMILARITY.
FT	DISULPID	556	BY SIMILARITY.
FT	DISULPID	564	BY SIMILARITY.
FT	DISULPID	577	BY SIMILARITY.
FT	DISULPID	579	BY SIMILARITY.
FT	DISULPID	592	BY SIMILARITY.
FT	DISULPID	596	BY SIMILARITY.
FT	DISULPID	649	BY SIMILARITY.
FT	DISULPID	671	BY SIMILARITY.
FT	DISULPID	712	BY SIMILARITY.
FT	DISULPID	719	BY SIMILARITY.
FT	DISULPID	732	BY SIMILARITY.
FT	DISULPID	734	BY SIMILARITY.
FT	CARBONYD	96	N-LINKED (GCNAC. .) (POTENTIAL).
FT	CARBONYD	147	N-LINKED (GCNAC. .) (POTENTIAL).
FT	CARBOND	337	N-LINKED (GCNAC. .) (POTENTIAL).
FT	CARBOND	368	N-LINKED (GCNAC. .) (POTENTIAL).
FT	CARBOND	604	N-LINKED (GCNAC. .) (POTENTIAL).
SQ	SEQUENCE:	991 AA;	111607 MW; 68A1847733A0BB9E CRC64;
Query Match	26.0%; Score 224; DB 1; Length 991;		
Best Local Similarity	33.6%; Pred. No. 3 3e-15;		
Matches	43; Conservative 27; Mismatches 16; Indels 2; Gaps 2;		
Oy	26 GRBKQTSETQSVQCGTWTKAEGGIFTSPNYPSPKVPDRQIVIIRAPQCIELYFD	85	
Db	751 GCRHKVTS-----GTTSPNWPDKPSKPKCTWAISSTRHRVKLFV	795	
Oy	86 EKYSIESPWECKEDHIEVRDGPGFSPPTIGRCCQONPVVSGRFLWIKFADGELES	145	
Db	796 E-MDIESOPECAYDHLEVFDGRDAKAPVILGRFCGSKKEPVLATGNMPLRIVSDNSVQR	854	
Oy	146 MGPARYN 153		

FT VARSPLIC 824 986 /FTId=VSP_005469.
 FT Missing (in isoform EMLP1-7).
 FT /FTId=VSP_005470.
 PT CONFLICT 748 748 D -> N (IN REF. 4).
 PT 934 934 R -> S (IN REF. 4).
 SQ SEQUENCE 986 AA; 111248 MW; F83201913AC3GBEA CRC64;
 Query Match 25.6%; Score 220.5; DB 1; Length 986;
 Best Local Similarity 38.2%; Pred. No. 7.6e-15;
 Matches 39; Conservative 24; Mismatches 38; Indels 1; Gaps 1;
 Oy 51 SPIGRCPGQONPPVIKSSRLWIKFADGELIESNGFSAR 152
 Db 756 GNTSPNPKDVKPSKCBETWAISSTPCHRVLKLTME-MDIESQPCAYDILEVFDGDKA 814
 Qy 111 APVLGSPCGSKRKEPVULATGSRMFLRFYSNSVQRKGFAQSH 856
 Db 815 APVLGSPCGSKRKEPVULATGSRMFLRFYSNSVQRKGFAQSH 856

RESULT 9

TLD_BRARE STANDARD; PRT; 1022 AA.

ID TLD_BRARE STANDARD; PRT; 1022 AA.

AC 057460; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Dorsal-ventral patterning tollloid protein precursor (EC 3.4.24.-)
 DE (Mini fin protein)
 GN Tollloid OR TLD OR MFN.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN [1] - TAXID=7955;
 RP *
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC
 RX
 MEDLINE-9805457; PubMed=9395394;
 RA Blader P., Rastegar S., Fischer N., Strähle U.;
 RT "Cleavage of the BMP-4 antagonist chordin by zebrafish Tollloid.";
 RL Science 278:1937-1940(1997).
 RN [2]
 FT FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE-99307076; PubMed=10375503;
 RA Connors S.A., Trout J.J., Bakker M., Mullins M.C.;
 RT "The role of tollloid/minifin in dorsoventral pattern formation of the
 zebrafish embryo.";
 RL Development 126:3119-3130 (1999).
 CC -!- FUNCTION: Required for patterning ventral tissues of the tail. May
 increase bone morphogenetic protein (BMP) activity at the end of
 gastrulation by proteolytic cleavage of chordin and release of BMP
 from inactive complexes.
 CC -!- TISSUE SPECIFICITY: During gastrulation, accumulates around the
 closing blastopore with greater expression ventrally. At the
 animal pole, expressed in the ectoderm flanking the anterior
 neural plate. At the 10-somite stage, expressed in the developing
 tailbud and cranial neural crest. At the 20-somite stage, also
 expressed in the hematopoietic system.
 CC -!- SIMILARITY: Belongs to peptidase family M12A.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 5 CUB domains.
 CC
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 DR AF027596; AAC63034.1; -.
 DR HSPB; P35555; 1EINN.

DR MEROPS; M12.015; -.
 DR ZFIN; ZDB-GENE-990415-265; tolloid.
 DR InterPro; IPR001052; Asx_hydroxyl_S.
 DR InterPro; IPR00859; CUB.
 DR InterPro; IPR01181; EGF_Ca.
 DR InterPro; IPR06209; EGF_Like.
 DR InterPro; IPR06025; Pept_M_Zn_BS.
 DR InterPro; IPR06026; Peptidase_M.
 DR InterPro; IPR01506; Peptidase_M12A.
 DR Pfam; PF00431; CUB; 5.
 DR Pfam; PF00008; EGF; 2.
 DR PRINTS; PR00480; ASTACIN.
 DR SMART; SM0042; CUB; 5.
 DR SMART; SM00179; EGF_CA; 2.
 DR PROSITE; PS0035; ZINC; 1.
 DR PROSITE; PS0010; ASX_HYDROXYL; 2.
 DR PROSITE; PS0142; ZINC_Protease; 1.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS0026; EGF; 3; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
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 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS0118; EGF; 2.
 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
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 DR PROSITE; PS0119; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 2.
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 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS0118; EGF; 2.
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 DR PROSITE; PS50026; EGF; 3; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
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Db	478 DSGQIQSPNYPDDYRPSKECWVWRITVSEGYSVGLSF-QVFEIERHSDCAYDYLEVRDGLS	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
Db	537 ENSP1LIGRCGYKEDIRKSTNNLUWKKVFSGTUNKAGFAANF	580	CC -!- FUNCTION: Required for normal dorsal development. TLD may interact physically with DPP-C protein.
RESULT 10	TLD_DROME	STANDARD;	PT; 1057 AA.
ID	TLD_DROME	PRT;	1057 AA.
DT	01-MAY-1992 (Rel. 22, Created)		CC -!- MISCELLANEOUS: Mutations in TLD lead to a partial transformation of dorsal ectoderm into ventral ectoderm.
DT	15-MAR-2004 (Rel. 43, Last annotation update)		CC -!- SIMILARITY: Belongs to peptidase family M12A.
DE	Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-).		CC -!- SIMILARITY: Contains 2 EGF-like domains.
GN	TLD OR CGE868.		CC -!- SIMILARITY: Contains 5 CUB domains.
OS	<i>Drosophila melanogaster</i> (Frucht fly).		CC -!- SIMILARITY: Contains 2 EGF-like domains.
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.		CC -!- SIMILARITY: Contains 2 EGF-like domains.
OC	NCBI_TAXID=7277;		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RN	[1]		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RC	SEQUENCE FROM N.A.		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RX	STRAIN=Canton-S;		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RX	MEDLINE=92034970; PubMed=1840509;		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RA	Shimline M.J., Ferguson E.L., Childs S.R., O'Connor M.B.;		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RT	"The <i>Drosophila</i> dorsal-ventral patterning gene tolloid is related to human bone morphogenetic protein 1.";		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RL	Cell 67:469-481(1991).		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RN	[2]		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RP	SEQUENCE FROM N.A.		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RX	MEDLINE=93124373; PubMed=7600363;		CC -!- SIMILARITY: Contains 2 EGF-like domains.
RA	Adams M.D., Celtniker S.E., Holt R.A., Evans C.A., Gocayne J.D., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.Y.-H., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers J.H.C., Blazquez R.G., Champé M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbavonyi A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balwol R.M., Basu A., Baxtarkaroglu I., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakow S., Borovka D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra T., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Gang N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPheron D., Merkulov G., Milashina N.V., Moarry C., Morris J., Moskrafi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paciorek J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).

RA	Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
RA	Zhang L.,	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
FT	DOMAIN	127	329
FT	DOMAIN	330	467
FT	DOMAIN	468	580
FT	DOMAIN	581	621
FT	DOMAIN	624	742
FT	DOMAIN	743	783
FT	DOMAIN	787	899
FT	DOMAIN	900	1016
FT	DOMAIN	221	222
FT	ACT_SITE	222	225
FT	METAL	225	231
FT	METAL	231	237
FT	SITE	235	237
FT	SITE	315	317
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
RA	Zhang L.,	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
FT	DOMAIN	127	329
FT	DOMAIN	330	467
FT	DOMAIN	468	580
FT	DOMAIN	581	621
FT	DOMAIN	624	742
FT	DOMAIN	743	783
FT	DOMAIN	787	899
FT	DOMAIN	900	1016
FT	DOMAIN	221	222
FT	ACT_SITE	222	225
FT	METAL	225	231
FT	METAL	231	237
FT	SITE	235	237
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	536	RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
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FT	DISULFID	330	380	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 2 F5/8 type C domains.
FT	DISULFID	407	429	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 1 MAM domain.
FT	DISULFID	468	495	BY SIMILARITY.	CC	-----
FT	DISULFID	522	544	BY SIMILARITY.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	DISULFID	585	596	BY SIMILARITY.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
FT	DISULFID	592	605	BY SIMILARITY.	CC	use by non-profit institutions as long as its content is in no way
FT	DISULFID	607	620	BY SIMILARITY.	CC	modified and this statement is not removed. Usage by and for commercial
FT	DISULFID	624	652	BY SIMILARITY.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/)
FT	DISULFID	683	706	BY SIMILARITY.	CC	or send an email to license@isb-sib.ch).
FT	DISULFID	747	758	BY SIMILARITY.	CC	-----
FT	DISULFID	754	767	BY SIMILARITY.	CC	-----
FT	DISULFID	769	782	BY SIMILARITY.	DR	DR EMBL; AF016296; AAC33371; -.
FT	DISULFID	787	813	BY SIMILARITY.	DR	HSSP; P12259; ICZT.
FT	DISULFID	840	862	BY SIMILARITY.	DR	InterPro; IPR00859; CUB.
FT	DISULFID	900	930	BY SIMILARITY.	DR	InterPro; IPR00421; F58_C.
FT	DISULFID	957	979	BY SIMILARITY.	DR	InterPro; IPR008979; Gal bind like.
FT	CARBHYD	166	166	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	InterPro; IPR00998; MAM_domain.
FT	CARBHYD	431	431	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	Pfam; PF00754; F5_F8_type_C; 2.
FT	CARBHYD	533	533	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	Pfam; PF00622; MAM_I.
FT	CARBHYD	634	634	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	PRINTS; PR00024; MANDOMATN.
FT	CARBHYD	667	667	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	SMART; SM0042; CUB; 2.
FT	CARBHYD	781	781	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	SMART; SM0023; FAS8C; 2.
FT	CARBHYD	854	854	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	SMART; SM00137; MAM; 1.
FT	CARBHYD	908	908	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	PROSTE; PS01180; CUB; 2.
FT	SEQUENCE	1057	AA;	120575 MW; 76F4B3RB7996FBA CRC64;	DR	PROSTE; PS01285; FAS8C_1; 2.
QY				25.2%; Score 217.5; DB 1; Length 1057;	DR	PROSTE; PS0186; FAS8C_2; 2.
QY				Best Local Similarity 38.4%; Pred. No. 1.7e-14; Indels 1; Gaps 1;	DR	PROSTE; PS50022; FAS8C_3; 2.
Db		466		VVCGGGIPLKLTQDOSIDSPNPYFMDYKPEWTRAPDNQVALF-QSELEKRHDGCAV 524	DR	PROSTE; PS00740; MAM_1; 1.
QY		99		DHEFRDGPGFPSPIGRGRGQQNPPVIEKGRFLWIKFADGELESMGNSA 150	DR	PROSTE; PS50060; MAM_2; 1.
Db		525		DFEVRDQGNSDSRJGRFCFOCDKLPNIKRSQNMWIFVSDSSVQKGPSA 576	DR	Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
RESULT 11				KW SIGNAL 1 21 POTENTIAL.	FT	CHAIN 22 922 NEUROPILIN-1.
NRPL_RAT	ID = NRP1_RAT		STANDARD;	DOMAIN 22 922 EXTRACELLULAR (POTENTIAL).	FT	DOMAIN 22 855 POTENTIAL.
AC Q90WJ9;			PRT; 922 AA.	TRANSMEM 856 880 CYTOPLASMIC (POTENTIAL).	FT	DOMAIN 881 922 MAM.
DT	16-OCT-2001 (Rel. 40, Last sequence update)			DOMAIN 147 265 PROBABLE.	FT	DISULFID 27 141 CUB 1.
DT	16-OCT-2001 (Rel. 40, Last sequence update)			DOMAIN 275 424 F5/8 TYPE C 1.	FT	DISULFID 147 173 PROBABLE.
DT	28-FEB-2003 (Rel. 41, Last annotation update)			DOMAIN 431 583 F5/8 TYPE C 2.	FT	DISULFID 206 228 PROBABLE.
DB	Neuropilin-1 precursor (vascular endothelial cell growth factor 165 receptor).			DISULFID 431 583 BY SIMILARITY.	FT	DISULFID 275 424 BY SIMILARITY.
GN	NRPL			DISULFID 431 583 BY SIMILARITY.	FT	DISULFID 150 150 BY SIMILARITY.
OS	Rattus norvegicus (Rat).			DISULFID 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			DISULFID 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.			DISULFID 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).
OX	NCBI_TAXID=10116;			DISULFID 922 AA; 103082 MW; CC6F2R2AD038BF2E CRC64;	SQ	SEQUENCE 922 AA; 103082 MW; CC6F2R2AD038BF2E CRC64;
RN	[1]			-----	-----	-----
RP	SEQUENCE FROM N_A:			-----	-----	-----
RC	STRAIN-Sprague-Dawley;			-----	-----	-----
RX	MEDLINE:97431085; PubMed=9288754;			-----	-----	-----
RA	Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,			-----	-----	-----
RA	Ginty D.D.;			-----	-----	-----
RT	"Neuropilin is a semaphorin III receptor.";			-----	-----	-----
RL	Cell 90:753-762(1997).			-----	-----	-----
CC	FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepellant activity of semaphorins. It binds to semaphorin 3A, the PLGF-2 isoform of PDGF, the VEGF-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis.			-----	-----	-----
CC	It may regulate VEGF-induced angiogenesis (By similarity).			-----	-----	-----
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			-----	-----	-----
CC	-!- TISSUE SPECIFICITY: Found in the embryonic nervous system.			-----	-----	-----
CC	-!- SIMILARITY: Belongs to the neuropilin family.			-----	-----	-----
CC	-!- SIMILARITY: Contains 2 CUB domains.			-----	-----	-----
RESULT 12				-----	-----	-----
	NRPL_MOUSE		STANDARD;	QY 37 KSVQCGWTWKAEGGIFTSPNPKYPPRECIVIEA-APROCYELFDEKYSIESWE 95	Db	37 KSVQCGWTWKAEGGIFTSPNPKYPPRECIVIEA-APROCYELFDEKYSIESWE 95
	ID = NRPL_MOUSE		PRT; 923 AA.	Db	96 CKFDMHETDGPGFSPSPIGRGRGQQNPPVIEKGRFLWIKFADGELESMGNSA 152	
	AC P97333;			Db	82 CKDYEVIDGENEGGRIGWKGFCGRKAPSPVSSGPFFIKFVSYDYEHGAGSIRY 138	
	01-NOV-1997 (Rel. 35, Created)					

01-NOV-1997 (Rel. 35, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update)

DISULFID 82 104 PROBABLE.

DISULFID 147 173 PROBABLE.

DISULFID 206 228 PROBABLE.

DISULFID 275 424 BY SIMILARITY.

DISULFID 431 583 BY SIMILARITY.

CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).

NCBI_TAXID=10050; RN [1]

RP SEQUENCE FROM N.A.

STRAIN=BALB/C; TISSUE=Embryonic brain;

MEDLINE=96353119; PubMed=87449368; RX

Kawakami A., Katsukawa T., Takagi S., Fujisawa H.; RL "Developmentally regulated expression of a cell surface protein, neuropilin, in the mouse nervous system.";

J. Neurobiol. 28:1-17(1995).

--!- FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsive activity of semaphorins. It binds to semaphorin 3A, the PLGF-2 isoform of pgf, the vEGFR-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis. It may regulate VEGF-induced angiogenesis (By similarity).

--!- SUBCELLULAR LOCATION: Type I membrane protein.

--!- TISSUE SPECIFICITY: Nervous system.

--!- SIMILARITY: Belongs to the neuropilin family.

--!- SIMILARITY: Contains 2 CUB domains.

--!- SIMILARITY: Contains 2 F5/8 type C domains.

--!- SIMILARITY: Contains 1 MAM domain.

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CC EMBL; D50086; BAA08789.11; --.

CC HSSP; P12259; 1CZT.

DR MGI:106206; NRP.

DR GO; GO:0017154; F:semaphorin receptor activity; IGI.

DR InterPro; IPR00559; CUB.

DR InterPro; IPR00421; FAS8_C.

DR InterPro; IPR008979; Gal_bind_like.

DR InterPro; IPR000998; MAM_domain.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00754; F5_F8_TYPE_C; 2.

DR Pfam; PP00629; MAM; 1.

DR PRINTS; PR00020; MAMDOMAIN.

DR SMART; SM00422; CUB; 2.

DR SMART; SM00331; FAS8C; 2.

DR SMART; SM0137; MAM; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; FAS8C; 1; 2.

DR PROSITE; PS01286; FAS8C; 2; 2.

DR PROSITE; PS50022; FAS8C; 3; 2.

DR PROSITE; PS00740; MAM; 1; 1.

DR PROSITE; PS50060; MAM; 2; 1.

KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat; KW Receptor.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 923 NEUROPILIN-1.

FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 857 879 POTENTIAL.

FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 27 141 CUB 1.

FT DOMAIN 147 265 CUB 2.

FT DOMAIN 275 424 F5/8 TYPE C 1.

FT DOMAIN 431 583 F5/8 TYPE C 2.

FT DOMAIN 645 811 MAM.

FT DISULFID 27 54 PROBABLE.

RESULT 13

RP SEQUENCE FROM N.A.

RC BMPH_STRPU STANDARD; PRT; 639 AA.

RX MEDLINE=98079; PMID=9162855;

RA Hwang S.-P.L., Partin J.S., Lemmarz W.-J., bone morphogenetic protein 1 characterization of a homolog of human bone morphogenetic protein 1 in the embryo of the sea urchin, Strongylocentrotus purpuratus.;"

RT Development 120:559-568 (1994).

RL CC --!- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in hatched blastula.

CC CC --!- DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.

CC CC --!- SIMILARITY: Belongs to Peptidase family M12A.

CC CC --!- SIMILARITY: Contains 1 EGF-like domain.

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CC DR EMBL; L23838; AA30081.1; --.

DR HSSP; P00736; 1AQK.

DR MEROPS; M12_005; --.

FT InterPro; IPR00152; Asx_hydroxyl_S.

DR InterPro; IPR00059; CUB.

DR InterPro; IPR00181; EGF_Ca.

DR InterPro; IPR00609; EGF_like.

DR InterPro; IPR00609; EGF_like.

DR InterPro; IPR006025; Pept_W_Zn_BS.

DR InterPro; IPR006026; Peptidase_M.

DR InterPro; IPR001506; Peptidase_M12A.

DR Pfam; PF01400; Astacin; 1.

DR Pfam; PF00431; CUB; 2.

QY 37 KSVQCGITWIKHAEAGGIFTSPNYPKSPYKPPDRCIYIEA-APROCIELYDEKYSIESWE 95

Db 23 RSDKGQTIKENPGYLTSFCYPHSYHPSKECWLQAPEPYQRITINFPNPHDLED-D 81

QY 96 CKFDHTEVDRDGPFGFSPILIGFCGQONPPVTKSSGRFLWIKIFPADDGELESWGSARY 152

Db 82 QKDYEVVIDEENEGGRLMWGCKIAPSVPVSGPFLPKFVSDYETHGAFSIRY 138

FT SEQUENCE 923 AA; 103020 MW; 0649BA170796808 CRC64;

Query Match 25.1%; Score 216; DB 1; Length 923; Best local similarity 40.2%; Pred. No. 2.1e+48; Indels 2; Gaps 2; CDR Matches 47; Conservative 20; Mismatches 48; Indels 2; Gaps 2; CDR

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL; L33799; AA61949.1; ALT_SEQ.
 DR EMBL; AB085456; AAC78800.1; -.
 DR EMBL; AF053356; AAD16041.1; -.
 DR EMBL; BC000574; AAH00574.1; -.
 DR EMBL; BC032205; AAH32205.1; -.
 DR Genew; HGNC:8738; PCOLCE.
 DR MIM; 600270; -.
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00643; C345C; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01189; NTR; 1.
 KW Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 449 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN.
 FT DOMAIN 37 149 CUB 1.
 FT DOMAIN 159 273 CUB 2.
 FT DOMAIN 318 437 NTR.
 FT SITE 287 288 CLEAVAGE.
 FT SITE 288 289 CLEAVAGE.
 FT SITE 293 294 CLEAVAGE.
 FT SITE 300 304 CLEAVAGE.
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 449 AA; 47972 MW; 3D88430150648796 CRC64;

Query Match 23.4%; Score 201.5; DB 1; Length 449;
 Best Local Similarity 37.1%; Pred. No. 2.9e-13;
 Matches 53; Conservative 20; Mismatches 57; Indels 13; Gaps 5;

QY 16 IHLISGATKKGKIKQTSETIQSVQCGWTKHAEGGIFTSPVYP-SXPPDPRECIVIEA 74
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 143 LAMYSGRATSGTHHQF-----CGGRLEKAQGTL-TTPNWPESSYPPGICSWHTIA 192

QY 75 APROCIETYDEKYSIESPWECKFDHIEVRDGPFG-FSPIIISRGFCQONPPVIKSSGFL 133
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 193 PPKQVIALTF-EKFDLDTYCRYDS/SVNGAVSDDSRRIKFCGDAVPGSISSEGEL 251

QY 134 WKPFPADDBLESMSFSARYNFTP 156
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 252 LWQFVSDLSVTADGFSASVYKTLP 274

RESULT 15

NPBP1_XENLA STANDARD; PRT; 928 AA.

ID _NPBP1_XENLA STANDARD; PRT; 928 AA.

AC P28824;

DT 01-DEC-1992 (Rel. 24, Created)

DT DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT DT 2004-04 (Rel. 43, Last annotation update)

DR Neuropilin-1 precursor (A5 protein) (A5 antigen).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

OC Xenopodinae; Xenopus.

OX NCBI_TAXID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MIDDLEN=91337458; PubMed=1908252;

RA Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;

"The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";
 RT RT
 RL Neuron 7:295-307 (1991).
 CC -!- FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorrepulsive activity of semaphorins (By similarity). Presumed to be involved in the neuronal recognition between the optic nerve fibers and the visual centers.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Retinal ganglion cells and visual center neurons.
 CC -!- SIMILARITY: Belongs to the neuropilin family.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 1 MAM domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; D10467; BAM01260.1; -.
 DR HSSP; P12259; ICZT.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR00421; FAS8_C.
 DR InterPro; IPR00579; Gal bind like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR PRINTS; PR00020; MAM_DOMAIN.
 DR SMART; SM00231; FAS8C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FAS8C_1; 2.
 DR PROSITE; PS01286; FAS8C_2; 2.
 DR PROSITE; PS00022; FAS8C_3; 2.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor; Antigen.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 928 NEUROPIPIN-1.
 FT DOMAIN 22 860 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 861 883 POTENTIAL.
 FT DOMAIN 884 928 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 27 141 CUB 1.
 FT DOMAIN 147 265 CUB 2.
 FT DOMAIN 275 424 F5/8 TYPE C 1.
 FT DOMAIN 431 584 F5/8 TYPE C 2.
 FT DOMAIN 646 812 MAM.
 FT DISULFID 27 54 PROBABLE.
 FT DISULFID 82 104 PROBABLE.
 FT DISULFID 147 173 PROBABLE.
 FT DISULFID 206 228 PROBABLE.
 FT DISULFID 275 424 BY SIMILARITY.
 FT DISULFID 431 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 928 AA; 103416 MW; AF6B323B024C789D CRC64;

Query Match 23.0%; Score 198.5; DB 1; Length 928;
 Best Local Similarity 32.4%; Pred. No. 1.4e-12;
 Matches 44; Conservative 26; Mismatches 53; Indels 13; Gaps 3;

Search completed: May 18, 2004, 18:22:52
Job time : 18 secs

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GenCore version 5.1.6
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ALIGNMENTS

TSG-6 homolog PS4
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
UVS-2 protein - AF
hypothetical prote
membrane-bound arg
oviductin (EC 3.4.
hypothetical prote
hypothetical prote
LDL receptor-relat
LDL receptor relat
spinal cord-derive
hypothetical prote
spinal cord-derive

OM protein - protein search, using sw model
Copyright (c) 1993 - 2004 Compugen Ltd.
GenCore version 5.1.6
Run on: May 18, 2004, 18:21:16 ; Search time 21 Seconds
(without alignments)
723.427 Million cell updates/sec
Title: US-09-887-593A-2
Perfect score: 862
Sequence: 1 MIGRSVLHTVAVSLIILHS ADGEALESMGFSARVNFTPGK 158
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:	283366	ALIGNMENTS
Minimum DB seq length:	0	JC7985
Maximum DB seq length:	2000000000	brain-specific CUB and LDLa domain-containing transmembrane protein, BTCL1 protein - M
Post-processing:	Minimum Match 0%	C;Species: Mus musculus
Database :	PIR_78:*	C;Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
	1: pir1:*	C;Accession: JC7985; PC7228
	2: pir2:*	R;Michiganita, M.; Ikeda, T.; Nakashiba, T.; Ogawa, M.; Tashiro, K.; Honjo, T.; Doi, K.
	3: pir3:*	Biochem. Biophys. Res. Commun. 306: 680-686, 2003
	4: pir4:*	A;Title: A novel gene, BTCL1, encoding CUB and LDLa domains is expressed in restricted A;Reference number: JC7985; PMID:12810072
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	A;Accession: JC7985
Result No.	Score	% Match Length DB ID
		SUMMARIES
		Description
1	818	94.9 533 2 JC7985
2	260	30.2 321 2 T33161
3	227.5	26.4 3623 2 T08118
4	227.5	26.4 3623 2 T0456
5	227	26.3 707 2 JCC218
6	224	26.0 991 2 149540
7	220.5	25.6 986 2 B58788
8	217.5	25.2 1057 1 A32828
9	216.5	25.1 1464 2 S58384
10	211	24.5 730 1 BMH01
11	211	24.5 823 1 A58788
12	199.5	23.1 1070 2 T31069
13	199	23.1 579 2 C7629
14	198.5	23.0 927 1 JQ0948
15	197.5	22.9 449 2 A53362
16	193.5	22.4 402 2 JH0403
17	187.5	21.8 1594 2 T30549
18	178.5	20.7 699 1 I14763
19	172.5	20.0 2403 2 A59386
20	171.5	19.9 1524 2 T30337
21	170.5	19.8 597 2 S71352
22	164.5	19.1 2083 2 T42721
23	162.5	18.9 504 2 S56745
24	161.5	18.7 3871 2 T28212
25	162.5	17.7 705 1 C1HURP
26	151	17.5 275 2 JG6506
27	151	17.5 277 2 A41735
28	17.4	310 2 S41055
29	14.9	1290 2 A57190
		RESULT 2
		T33161
		hypothetical protein KO3E5.1 - Caenorhabditis elegans
		C;Species: Caenorhabditis elegans
		C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
		C;Accession: T33161
		R;Becker, M.; Graves, T.; Fronick, B.
		submitted to the EMBL Data Library, May 1998
		A;Description: The sequence of C. elegans cosmid KO3E5.
		A;Reference number: 2221294
		A;Accession: T33161

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA <K0Z>
A;Residues: 1-321 <BSC>
A;Cross-references: EMBL:AF034611; NID:93929528; PIDN: AAC82612.1; PID:93929529
C;Genetics:
A;Map position: 10p12
A;Gene: CESP; K03E5.1
A;Map position: 1
A;Introns: 25/1; 47/1; 84/2; 112/3; 131/3; 162/1; 197/1; 275/2
Query Match 30.2%; Score 260; DB 2; Length 321;
Best Local Similarity 43.5%; Pred. No. 6; 3e-19; Indels 8; Gaps 2;
Matches 50; Conservative 20; Mismatches 37; Indels 8; Gaps 2;
Qy 52 IFTSPNPKSKYPPRECIVIYEAPRQCIELYDEKYSIESPSW-----ECKFDHIEVR 104
Db 75 IFTSPNPKDFDYPNIDCVVHISRQPQHVVVKTHVVFHIESTVDKIDAGEEECPNDIEFR 134
Qy 105 DSGPGFSPITIGRFGQQNQPP-WTKSSGRFLWIKKFADGELESMGFSARYNFTPGK 158
Db 135 DGRYGFSPLIARFCGDRLPKREIRAVSGFLWIKPRSDMSMLEVOGFSAYATVPSK 189
RESULT 3
T08618 Intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
C;Accession: T08618
R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Karsen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5215-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A;Reference number: 216459; MUID:98148073; PMID:9478979
A;Accession: T08618
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <MOE>
A;Cross-references: EMBL:AF022247; NID:93834379; PIDN: AAC71661.1; PID:93834380
C;Genetics:
A;Gene: CUBILIN
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology <EGF>
C;Keywords: egg-yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
C;KeyWords: signal sequence #status predicted <SIG> #status predicted <MAT>
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted
F;7-33-164/Domain: EGF homology <EGF>
F;436-467/Domain: EGF homology <EGF>
Query Match 26.4%; Score 227.5; DB 2; Length 3623;
Best Local Similarity 35.1%; Pred. No. 2.1e-1; Indels 47; Mismatches 47; Gaps 9; Gaps 3;
Matches 46; Conservative 29; Mismatches 47; Indels 9; Gaps 3;
Qy 37 KSVQCG-TWTHAE-GGIFTSPNPKSKYPPRECIVIYEAPRQCIELYDEKYSIESPS 93
Db 2213 KSLACGGANVYIHDASDACYVTPNPHMPHADCIWILAPPETRQLQFEDRPFIEVT 2272
Qy 94 WECKFDHIEVRDGPFGSPITIGRFGQQNQPP-WTKSSGRFLWIKKFADGELESMGFSARYN 153
Db 2273 PNCTSNVYHLRDGVDSAPLISKPGTSLUPSSQWSSGHWYLRPDSNPTHVGFKAKYS 2332
Qy 154 F-----FTPGK 158
Db 2333 IAQCGGRVFGQ 2343
RESULT 5
JC2218 Procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N;Alternate name: bone morphogenic protein 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C;Accession: JC2218
R;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H. Gene 134, 257-261, 1993
A;Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein
A;Reference number: JC2218; MUID:94085787; PMID:8262384
A;Accession: JC2218
A;Molecule type: mRNA
A;Residues: 1-707 <MAE>
A;Cross-references: GB:112249; NID:9406540; PIDN: AAC16313.1; PID:9406541
C;Comment: This protein induces ectopic cartilage formation in vivo.
C;Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology; Cir/Cis
C;Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F;93-284/Domain: astacin homology <AST>
F;285-397/Region: complement 1r/s-like repeat
F;295-394/Domain: Cir/Cis repeat homology <CIR1>
F;398-510/Region: complement 1r/s-like repeat
F;398-507/Domain: Cir/Cis repeat homology <CIR2>
F;514-550/Domain: EGF homology <EGF>
F;554-663/Region: complement 1r/1s-like repeat
F;554-663/Domain: Cir/Cis repeat homology <CIR3>
F;62-105, 295, 326/Binding Site: carbohydrate (Asn) (covalent) #status predicted
F;177-180, 186, 235/Binding Site: zinc (His, His, His, Tyr) #status predicted
F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
RESULT 4
TO9456 Intrinsic factor-B12 receptor Cubilin precursor - human
C;Species: Homo sapiens (man) :
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C;Accession: TO9456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.;Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.
A;Reference number: 216677; MUID:98241400; PMID:9572993
A;Accession: TO9456
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-3623 <K0Z>
A;Cross-references: EMBL:AF034611; NID:93929528; PIDN: AAC82612.1; PID:93929529
C;Genetics:
A;Map position: 10p12
A;Gene: CESP; K03E5.1
A;Map position: 1
A;Introns: 25/1; 47/1; 84/2; 112/3; 131/3; 162/1; 197/1; 275/2
Query Match 30.2%; Score 260; DB 2; Length 707;
Best Local Similarity 40.2%; Pred. No. 3.7e-15; Indels 2; Gaps 2;
Matches 45; Conservative 18; Mismatches 47; Indels 2; Gaps 2;
Qy 41 CGTWTKHAEGGTSPNPKSKYPPRECIVIYEAPRQCIELYDEKYSIESPSWCKFDH 100
Db 398 CGEVVKDKSHT-QSNVYDPYRNCAKWKLSVSEGFHVGIFSF-QSFETERHDSCAYD 455
Qy 101 IERVDSGPFGSPITIGRFGQQNQPP-WTKSSGRFLWIKKFADGELESMGFSARY 152
Db 456 IBDGDSSETPLVGRCPGYDKPDDIKSNTQWIKVFDGSINKAGFSINY 507
RESULT 6

I49540
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollloid-like splice form - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
 Dev. Biol. 163, 175-183, 1994
 A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
 A;Reference number: I49540; MUID:94229342; PMID:8174772
 A;Accession: I49540
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residues: 1-991 <RGS>
 A;Cross-references: GB:L24755; NID:9439606; PIDN:AAA37306.1; PID:9439607
 A;Molecule type: mRNA
 C;Genetics:
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
 C;Keywords: hydrolase; metalloproteinase; zinc
 F;135-326-/domain: astacin homology <AST>
 F;56-592-/domain: EGF homology <EG1>
 F;595-705-/domain: C1r/C1s repeat homology <C1R>
 F;712-747-/domain: EGF homology <EG2>
 F;18-222-277-/Binding site: zinc (His, His, His, His, Tyr) #status predicted
 F;219/Active site: Glu #status predicted

Query Match 26.0%; Score 224; DB 2; Length 991;
 Best Local Similarity 33.6%; Pred. No. 1 le-14; Mismatches 43; Conservative 27; Indels 16; Gaps 2; Matches 43; Zinc (His, His, His, His, Tyr) #status predicted

Qy 26 GPKQQTSETQKVQCGTWWTKHAEGLFTSPNPYKSPPKPPRECIVYLTEAAPQCIELYFD 85
 • Db 751 GCBHKVFTS-----GTTSPNPDVKPSKKBTWAISSTPCHRVKLT 795

Qy 86 EKVISIEPSSWCKDHIEVRDGFPGFSPILGRFGQGQNPPIVIKSGRFLWIKIFADGELES 145
 • Db 796 E-MDIESQPECAYDHLVEPFGRDKAPAVLGRGSKKEPEPVATGNMFLRIVYSDNSVQR 854

Qy 146 MGFSARYN 153
 Db 855 KGFQASHS 862

RESULT 7
 B58788
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollloid-like splice form - human
 N;Alternate names: bone morphogenic protein 1, tolloid-like splice form
 C;Species: Homo sapiens (man)
 C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
 C;Accession: A37278; B58788
 R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1988
 A;Title: Novel regulators of bone formation: molecular clones and activities.
 A;Reference number: A37278; MUID:89072730; PMID:3201241
 A;Accession: A37278
 A;Molecule type: mRNA
 A;Residues: 1-707; 'ERKPAQPPGRGRPHQLKERVQKRNPQ' <W0Z>
 A;Cross-references: GB:M22488; NID:9179599; PIDN:AAA51633.1; PID:9179500
 R;Takahara, K.; Lyons, G.E.; Greenstein, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by the same gene
 A;Reference number: A58788; MUID:95096114; PMID:7798260
 A;Accession: B58788
 A;Molecule type: mRNA
 A;Residues: 703-96 <TAK>
 A;Cross-references: GB:L35279; NID:9619860; PIDN:AAAC41710.1; PID:9619861
 C;Function:
 C;Genetics:
 A;Gene: GDB: BMP1; BMP-1
 A;Cross-references: GDB:125203; OMIM:112264
 A;Map position: 8p21-8p21
 C;Function:
 A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type II
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
 C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g

F;1-22-/domain: signal sequence #status predicted <SIG>
 C;Species: Procollagen C-endopeptidase tollloid-like splice form #status predicted
 F;130-321-/domain: astacin homology <AST>
 F;322-431-/domain: C1r/C1s repeat homology <C1R>
 F;435-541-/domain: C1r/C1s repeat homology <C1R>
 F;551-587-/domain: EGF homology <EG1>
 F;591-700-/domain: C1r/C1s repeat homology <C1R3>
 F;707-741-/domain: EGF homology <EG2>
 F;747-856-/domain: C1r/C1s repeat homology <C1R4>
 F;860-973-/domain: C1r/C1s repeat homology <C1R5>
 F;91-142-332-363-599-Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;163-319-185-205-322-348-375-397-435-461-488-510-551-53, 55-572, 574-587, 591-617, 644-6
 F;213-217-223-272-/Binding site: zinc (His, His, His, His, Tyr) #status predicted
 F;214/Active site: Glu #status predicted
 C;Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F;565, 720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 25.6%; Score 220.5; DB 1; Length 986;
 Best Local Similarity 38.2%; Pred. No. 2.5e-14; Mismatches 39; Conservative 24; Indels 1; Gaps 1; Matches 39; Zinc (His, His, His, His, Tyr) #status predicted

Qy 51 GIFTSPNPKSPKPPRECIVYLTEAAPQCIELYFDKEYSIESPWECKDHIEVRDGFPGF 110
 • Db 756 GRTTSPNPKSPKSKTWAISSTPCHRVKLTME-MDIESQPECAYDHLVEFGRDAK 814

Qy 111 SPITRREGQKQPKVVKSGREWKIFADGELESMSGRFASARY 152
 • Db 815 APVLGRCFGSKKEPEPVATGSRMFLRIVYSDNSVQRGFQASH 856

RESULT 8
 A39288
 dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A39288
 R;Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
 Cell 67, 469-481, 1991
 A;Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
 A;Reference number: A39288; MUID:92034970; PMID:1840509
 A;Accession: A39288
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1057 <SH1>
 A;Cross-references: GB:MT6976; NID:9157305; PIDN:AAA28491.1; PID:9157306
 C;Genetics:
 A;Gene: FlyBase:tld
 A;Cross-references: FlyBase:FBgn003719
 C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat homology
 C;Keywords: duplication; hydrolase; metalloproteinase; zinc
 F;136-329-/domain: astacin homology <AST>
 F;352-464-/domain: C1r/C1s repeat homology <C1R1>
 F;468-578-/domain: C1r/C1s repeat homology <C1R2>
 F;585-620-/domain: EGF homology <EG1>
 F;624-740-/domain: C1r/C1s repeat homology <EG2>
 F;747-782-/domain: EGF homology <EG2>
 F;900-1013-Domain: C1r/C1s repeat homology <C1R3>
 F;221-225, 231, 280-/Binding site: zinc (His, His, His, His, Tyr) #status predicted
 F;222/Active site: Glu #status predicted

Query Match 25.2%; Score 217.5; DB 1; Length 1057;
 Best Local Similarity 38.4%; Pred. No. 5.6e-14; Mismatches 43; Zinc (His, His, His, His, Tyr) #status predicted
 Conservative 21; Indels 1; Gaps 1; Matches 43; Zinc (His, His, His, His, Tyr) #status predicted

Qy 39 VOOGTWTKAEGGLFTSPNPYKSPKPPRECIVYLTEAAPQCIELYFDKEYSIESPWECKF 98
 • Db 466 WVGCGDKLTKQSISDNPYKMDIMPKECWTRAFDNHQVALKE-QSFELERKHDCAV 524

Qy 99 DHLEVRDPGPGSPGSPGFRGFCGQNPPIVKKFFANGELLSMGFSA 150
 • Db 525 DFEVRDGNNHSRSRLIGRCFGDKLUPNIKTSNQMYIRFVSDSSVQKLGFA 576

RESULT 12

T31069 tollloid-BMP-1 like protein 1 - California sea hare

N;Alternate names: probable metalloprotease TBL-1

C;Species: Aplysia californica (California sea hare)

C;Accession: T31069 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000

R;Liu, Q.R.; Hattar, S.; Endo, S.; Macphee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es

J.; Neurosci. 17, 755-764, 1997

A;Title: A developmental gene (Tollolid/BMP-1) is regulated in Aplysia Neurons by treatment

A;Reference number: 220965; MUID:98007484; PMID:8987797

A;Accession: T31069 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Cross-references: EMBL:U57369; NID:gi189941; PID:gi189942; PIDN: AAC7485.1

C;Superfamily: dorsal-ventral patterning protein tollolid; astacin homology; C1r/C1s repeat

A;Residues: 1-1070 <LIU>

A;Molecule type: mRNA

A;Cross-references: 1-1070 <LIU>

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Cross-references: 1-1070 <LIU>

A;Molecule type: mRNA

A;Cross-references: 1-1070 <LIU>

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Cross-references: 1-1070 <LIU>

A;Molecule type: mRNA

A;Cross-references: 1-1070 <LIU>

A;Status: preliminary; translated from GB/EMBL/DDBJ

Db

256 GR 257 |:

RESULT 14

A5 antigen precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C;Accession: JH0466; JQ0548

R;Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.

Neuron 7, 295-307, 1991

A;Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology

A;Reference number: JH0466; MUID:91337458; PMID:1908252

A;Accession: JH0466

A;Molecule type: mRNA

A;Cross-references: GB:D10467; GB:D01077; NID:9222962; PIDN:BAA01260.1; PID:9222963

A;Experimental source: tadpole, brain

C;Comment: this protein has motifs homologous to complement components C1r and C1s and to

C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-97/Domain: C1r/C1s repeat homology <CIR1>

F;147-262/Domain: C1r/C1s repeat homology <CIR2>

F;274-424/Domain: discoidin I amino-terminal homology <DN1>

F;430-584/Domain: MM homology <MM>

F;861-883/Domain: transmembrane #status predicted <TMM>

F;150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.0%; Score 198.5; DB 1; Length 927;

Matches 44; Conservative 32.4%; Pred. No. 4.3e-12; Mismatches 53; Indels 13; Gaps 3;

QY 32 TSETOKSVQGTWTKHAEGGIFTSPNMPSKVPDRRCIYIEAAPP-QCTELYDEKYSI 90

Db 18 SSWSARNDKGCGDTKTTSPLSYLTSGAHPYSPSSGRCEWLTOAPHYQRTMINFNPHFDL 77

QY 91 RPSWCKFDHIEVRDGGPGGSPILGRFCGQONPPVVKSSGRFLWIKFFADGELESNGFSA 150

Db 78 EDR-ECKYDVTEVIGDNGNQNLQGKCYGKCIAPSPLVSTGSPSIFIRFVSDYETPGAFSI 136

QY 151 RY-----MFT 155

Db 137 RYEVFKTGPRCSRNF 152

Query Match 23.1%; Score 199; DB 2; Length 579;

Matches 29.1%; Pred. No. 2.2e-12; Mismatches 53; Conservative 25; Indels 34; Gaps 6;

QY 7 VLUHTASLILHLSATKKG-----TEKOTTSFQSTQCGTWTKHAGGI-- 52

Db 80 LIGHVIAAILAQOLQAPPGSASHSPPLASGGLTTTTPPTTSQAGTPKGQOBGSVSPS 139

QY 53 -----FTSNIPKSKPPDRRCIYIEAAPP-QCTELYDEKYSI 97

Db 140 PQQSGGGLGSPGPFRFESSNPYDPYRPNHWHIQVATTAQKLKIALSRSVACL 198

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Cross-references: 1-449 <TAK>

C;Genetics:

A;Accession: A55362

A;Cross-references: GB:P01CE

A;Map position: 7q21.3-q22

A;Cross-references: OMIM:600270

C;Keywords: extracellular protein; glycoprotein; pyroglutamic acid

F;26-449/Product: #status predicted <MA1>

F:37-146/Domain: C1r/C1s repeat homology <C1R>
F:159-270/Domain: C1r/C1s repeat homology <C1R2>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.9%; Score 197.5; DB 2; Length 449;
Best Local Similarity 36.4%; Pred. No. 2.4e-12;
Matches 52; Conservative 21; Mismatches 57; Index 13; Gaps 5;
Matches 52; Conservative 21; Mismatches 57; Index 13; Gaps 5;

Qy	16	IHLSGATKKKEKOTSETOKSVQCGTWTKHAEGGIFTSPNYP-SKYPPDRECIVTEA	74
	:	: :	
Db	143	LWYSGRATSSEHQF-----COGRERAKQGIL-TPNWPSDYPROISCSWHILA	192
	:	: :	
Qy	75	APROCTELVPRKYSPEPSWCKEDHIEVRDGPFG-FSPPIIGRFEGQONPVIKSGRL	133
	:	: : : : : : : : : : : : : : : : : : : :	
Db	193	PPDQVALTF-BKFOLERPDTYCRYDSVSVFENGAVSDDSRRLGKFCGDAVPGSISSEGNEI	251
	:	: : : : : : : : : : : : : : : : : : : :	
Qy	134	WIKFFADGELESMGFSARYNTP	156
	:	: : : : : : : : : : : : : : : : : : :	
Db	252	LVQFVSDLSVTADGESASYKILP	274

Search completed: May 18, 2004, 18:24:52
Job time : 22 secs

Query Match 98.7%; Score 851; DB 13; Length 533;
 Best Local Similarity 100.0%; Pred. No. 3.4e-85; Mismatches 0; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0;

Qy 121 QNPPVIKSSGRFLWIKFFADGELESMGFSARYNFTP 158
 Db 121 QNPPVIKSSGRFLWIKFFADGELESMGFSARYNFTP 158

RESULT 2
 US-10-138-588-38
 ; Sequence 38, Application US/10138588
 ; Publication No. US20040018534A1
 GENERAL INFORMATION:
 APPLICANT: Absobrook et al.
 TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
 FILE REFERENCE: 21402-347A
 CURRENT APPLICATION NUMBER: US/10/138,588
 CURRENT FILING DATE: 2002-05-01
 PRIOR APPLICATION NUMBER: 60/288,395
 PRIOR FILING DATE: 2001-05-03
 PRIOR APPLICATION NUMBER: 60/308,901
 PRIOR FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: 60/313,388
 PRIOR FILING DATE: 2001-08-17
 PRIOR APPLICATION NUMBER: 60/324,757
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: 60/288,900
 PRIOR FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 203
 SEQ ID NO: 38
 LENGTH: 526
 TYPE: PRT
 ORGANISM: Homo sapiens
 ;US-10-138-588-38

Query Match 98.7%; Score 851; DB 15; Length 526;
 Best Local Similarity 100.0%; Pred. No. 3.4e-85; Mismatches 0; Indels 0; Gaps 0;
 Matches 156; Conservative 0;

Qy 1 MHGRSVLHTIVASLTLILHLSATKKGTEKQTSETOKSVOGTMWKAEGGIFTSPNYS 60
 Db 1 MHGRSVLHTIVASLTLILHLSATKKGTEKQTSETOKSVOGTMWKAEGGIFTSPNYS 60

RESULT 4
 US-10-162-435-27
 ; Sequence 27, Application US/10162435
 ; Publication No. US20030096305A1
 GENERAL INFORMATION:
 APPLICANT: Meyers, Rachel
 APPLICANT: Gluckmann, Maria Alexandra
 APPLICANT: Curtis, Rory A.J.
 APPLICANT: Kapeller-Libermann, Rosana
 APPLICANT: Bandaru, Rajasekhar
 APPLICANT: Leiby, Kevin R.
 TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
 CELL SURFACE PROTEIN FAMILY MEMBERS
 FILE REFERENCE: 10448-189001
 CURRENT APPLICATION NUMBER: US/10/162,435
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: US 09/836,499
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: PCT/US01/12420
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: US 60/197,507
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/891,008
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: PCT/US01/19963
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: US 60/214,220
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 09/860,868
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: PCT/US01/16013
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/205,674
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/886,429
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: PCT/US01/20055
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/213,963
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 10/041,406
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: PCT/US02/00275
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/260,286
 PRIOR FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: US 09/934,268
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: PCT/US01/41811
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/226,612
 PRIOR FILING DATE: 2000-08-21
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 27
 LENGTH: 533
 TYPE: PRT
 ORGANISM: Homo sapiens
 ;US-10-041-406-2

Query Match 98.7%; Score 851; DB 13; Length 533;
 Best Local Similarity 100.0%; Pred. No. 3.4e-85; Mismatches 0; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0;

Qy 1 MHGRSVLHTIVASLTLILHLSATKKGTEKQTSETOKSVOGTMWKAEGGIFTSPNYS 60
 Db 1 MHGRSVLHTIVASLTLILHLSATKKGTEKQTSETOKSVOGTMWKAEGGIFTSPNYS 60

RESULT 5
 US-10-162-435-27
 ; Sequence 27, Application US/10162435
 ; Publication No. US20030096305A1
 GENERAL INFORMATION:
 APPLICANT: Bandaru, Rajasekhar
 TITLE OF INVENTION: A NOVEL CUB DOMAIN CONTAINING PROTEIN FAMILY MEMBER AND USES THEREOF
 FILE REFERENCE: 10448-13001
 CURRENT APPLICATION NUMBER: US/10/041,406
 PRIOR APPLICATION NUMBER: 60/260,286
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 09/934,268
 PRIOR FILING DATE: 2001-01-08
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 27
 LENGTH: 533
 TYPE: PRT
 ORGANISM: Homo sapiens
 ;US-10-041-406-2

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-162-435-27

Query Match 98.7%; Score 851; DB 14; Length 533;
Best Local Similarity 100.0%; Pred. No. 3.4e-85; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTHGRSVHHLVAVASLILHSGATKKGEBKQTSETOKSQCGTWKHBGGIFTSPNYP 60
Db 1 MIGRSVHLVAVASLILHSGATKKGEBKQTSETOKSQCGTWKHBGGIFTSPNYP 60

Qy 61 KPPDREQLVIEBAAPROCIYFDEKYSIESWECRDHIEVRDGPGFSIIGRCGQ 120
Db 61 KYPDPDRCIVIEBAAPROCIYFDEKYSIESWECRDHIEVRDGPGFSIIGRCGQ 120

Qy 121 QNPPIVKSSGRFWIKFADGELESMSGRSARNTPG 156
Db 121 QNPPIVKSSGRFWIKFADGELESMSGRSARNTPG 156

RESULT 5
US-09-764-853-653
; Sequence 653, Application US/09764853
; Patent No. US2002009672A1

GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PIZ06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; PRIORITY: Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 653
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-853-653

RESULT 7
US-09-764-881-116
; Sequence 116, Application US/09764881
; Publication No. US2002008683A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PIZ207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; PRIORITY: Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-881-116

RESULT 6
US-09-764-881-116
; Sequence 116, Application US/09764881
; Publication No. US2002008683A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PIZ207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; PRIORITY: Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 141

RESULT 5
US-09-764-881-116
; Sequence 116, Application US/09764881
; Publication No. US2002008683A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PIZ207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; PRIORITY: Prior application number: 09/764,881
; PRIORITY: Prior filing date: 2001-01-17
; PRIORITY: Prior application number: 60/179,065
; PRIORITY: Prior filing date: 2000-01-31
; PRIORITY: Prior application number: 60/180,628
; PRIORITY: Prior filing date: 2000-02-04
; PRIORITY: Prior application number: 60/214,886

PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-747-116

Query Match 55.6%; Score 479; DB 15; Length 141;
Best Local Similarity 66.1%; Pred. No. 8.4e-45;
Matches 80; Conservative 21; Mismatches 20; Indels 0; Gaps 0;

QY 38 SVOCGTWTWTKHAEAGGIFTSPNPKSPKYPDRECYTIEAAPRQCILYFDKYSIEPSWCK 97
Db 9 ATOCGIVWRTSNGGHFASPNYPSYPPNKECITYLEAAPRQBELTFDEHYIPESSFCR 68

QY 98 FDHIEVRGCPFGISPIGRFCGQNPPVIKSGRFLWIKFFANGELSMGFSARVNFTG 157
Db 69 FDHIEVRDGPFGSPLIDRYCGVSKPLRSTGRFMWIKPSDRELEGFGRAKYSFPG 128

QY 158 K 158
Db 129 K 129

*

RESULT 9
US-10-276-774-2238
; Sequence 2238, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1 e1 Nucleic Acids and Polypeptides
; CURRENT APPLICATION NUMBER: US10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2238
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2238

Query Match 54.5%; Score 470; DB 12; Length 525;
Best Local Similarity 54.9%; Pred. No. 4.4e-43;
Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVHII--VASHLHSATKKGTEKQQTSETOKSVQOCTWTWTKHAEAGGIFTSPNPKSP 63
Db 8 SVKLVLITVWVEGIAAQTKDQGQNIKIHPATOGIWVRTSNGGHFASPNYPSY 67

QY 64 PDRECYTIEAAPRQCILYFDKYSIIPSWECKFDHTEVRODPFGFSPIGRFCGQNP 123
Db 68 PNKECITYLEAAPRQBELTFDEHYIPESSFCRFDHIEVRDGPFGSPLIDRYCGVSKP 127

QY 124 PVIKSGRLWIKFADGELEMGSFSAVNFTG 156
Db 128 PLRSTGRFMWIKPSDRELEGFGRAKYSFPG 160

*

RESULT 11
US-10-145-127-114
; Sequence 114, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEAR
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-03-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 114
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-114

Query Match 54.5%; Score 470; DB 12; Length 525;
Best Local Similarity 54.9%; Pred. No. 4.4e-43;
Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVHII--VASHLHSATKKGTEKQQTSETOKSVQOCTWTWTKHAEAGGIFTSPNPKSP 63
Db 8 SVKLVLITVWVEGIAAQTKDQGQNIKIHPATOGIWVRTSNGGHFASPNYPSY 67

QY 64 PDRECYTIEAAPRQCILYFDKYSIIPSWECKFDHTEVRODPFGFSPIGRFCGQNP 123
Db 68 PNKECITYLEAAPRQBELTFDEHYIPESSFCRFDHIEVRDGPFGSPLIDRYCGVSKP 127

QY 124 PVIKSGRLWIKFADGELEMGSFSAVNFTG 156
Db 128 PLRSTGRFMWIKPSDRELEGFGRAKYSFPG 160

*

RESULT 11
US-10-145-127-114
; Sequence 114, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel K
 APPLICANT: Watanae, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C252

CURRENT APPLICATION NUMBER: US/10/145,127

CURRENT FILING DATE: 2002-05-13

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 114

LENGTH: 525

TYPE: PRT

ORGANISM: Homo Sapien

US-10-145-127-114

RESULT 12

Query Match 54.5%; Score 470; DB 12; Length 525;
 Best Local Similarity 54.9%; Pred. No. 4-4e-43;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVLH--VSLVLTILHLSGATKKGTEKQTSETOKSVQCGTWTKHAEGGIFTSPNYPKYP 63
 Db 8 SVLKVLVLTIVLVEGIAVAQKTQDGQNIGIKHITPATOCGIWVRNNGHFASPNYPDSYP 67

QY 64 PDRDCIYIEAARPCIELYDEKYSIESWECKFDHIEVRDGFPGFSPIIGRCQQNP 123
 Db 68 PNKCIVILEAAPRQEILTDFHYTIPSFCRFDHLVRDGFPGFSPLIDRYCVKSP 127

QY 124 PVIKSSGRFLWIKEFFADGELESMGFFSARINFTP 156
 Db 128 PLIRSTGFMWMKESSEBEELEGIFGRAKYSFIP 160

RESULT 13

US-10-143-118-114

Sequence 114, Application US/10143118

Publication No. US20040038335A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filavroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Godowski, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Godowski, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel K

APPLICANT: Watanae, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C228

CURRENT APPLICATION NUMBER: US/10/143,118

CURRENT FILING DATE: 2002-05-09

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 114

LENGTH: 525

TYPE: PRT

ORGANISM: Homo Sapien

US-10-143-118-114

RESULT 14

Query Match 54.5%; Score 470; DB 12; Length 525;
 Best Local Similarity 54.9%; Pred. No. 4-4e-43;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVLH--VSLVLTILHLSGATKKGTEKQTSETOKSVQCGTWTKHAEGGIFTSPNYPKYP 63
 Db 8 SVLKVLVLTIVLVEGIAVAQKTQDGQNIGIKHITPATOCGIWVRNNGHFASPNYPDSYP 67

QY 64 PDRDCIYIEAARPCIELYDEKYSIESWECKFDHIEVRDGFPGFSPIIGRCQQNP 123
 Db 68 PNKCIVILEAAPRQEILTDFHYTIPSFCRFDHLVRDGFPGFSPLIDRYCVKSP 127

QY 124 PVIKSSGRFLWIKEFFADGELESMGFFSARINFTP 156
 Db 128 PLIRSTGFMWMKESSEBEELEGIFGRAKYSFIP 160

RESULT 14

US-10-144-993-114

Sequence 114, Application US/10144993

Publication No. US20040038336A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 114
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo Sapien
 ; US-10-144-993-114
 ;
 Query Match 54.5%; Score 470; DB 12; Length 525;
 Best Local Similarity 54.9%; Pred. No. 4.4e-43;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
 APPLICANT: Tomas Daniel K.
 APPLICANT: Watanabe,Colin K
 APPLICANT: Wood,William
 APPLICANT: Zhang, Zemin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3330R1C449
 CURRENT APPLICATION NUMBER: US/10/144,993
 CURRENT FILING DATE: 2002-05-13
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 114
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo Sapien
 ; US-10-158-787-114
 ;
 Query Match 54.5%; Score 470; DB 12; Length 525;
 Best Local Similarity 54.9%; Pred. No. 4.4e-43;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
 APPLICANT: Tomas Daniel K.
 APPLICANT: Watanabe,Colin K
 APPLICANT: Wood,William
 APPLICANT: Zhang, Zemin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3330R1C449
 CURRENT APPLICATION NUMBER: US/10/158,787
 CURRENT FILING DATE: 2003-04-03